B57

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7 : C12Q 1/68, C12N 15/00, 15/09, 15/63, 15/86 | A1

(11) International Publication Number: WO 00/55375

(43) International Publication Date: 21 September 2000 (21.09.00)

(21) International Application Number: PCT/US00/07285

(22) International Filing Date: 17 March 2000 (17.03.00)

(30) Priority Data:

60/124,916	17 March 1999 (17.03.99)	US
60/124,808	17 March 1999 (17.03.99)	US
60/149,639	17 August 1999 (17.08.99)	US
60/157,247	1 October 1999 (01.10.99)	US
60/167,824	29 November 1999 (29.11.99)	US
60/182,711	15 February 2000 (15.02.00)	US

(71) Applicant: ALPHAGENE, INC. [US/US]; 260 West Cummings Park, Woburn, MA 01801 (US).

(72) Inventors: VALENZUELA, Dario; 1081 Hill Road, Boxborough, MA 01719-1010 (US). YUAN, Olive; 292 Mystic Street, Arlington, MA 02174 (US). HOFFMAN, Heidi; 90 Houghton Mill Road, Lunenburg, MA 01462 (US). HALL, Jeff; 4 Alderwood Drive, Stratham, NH 03885 (US). RAPIEJKO, Peter; 63 Old Grafton Road, Upton, MA 01568 (US).

(74) Agent: SPRUNGER, Suzanne, A.; American Home Products Corporation, Patent & Trademark Dept. – 2B, One Campus Drive, Parsippany, NJ 07054 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

With international search report.
Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract

Novel polynucleotides and the proteins encoded thereby are disclosed.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

This application is a continuation-in-part of the following applications:

(1) provisional application Ser. No. 60/124,916, filed March 17, 1999;

(2) provisional application Ser. No. 60/124,808, filed March 17, 1999;

(3) provisional application Ser. No. 60/149,639, filed August 17, 1999;

(4) provisional application Ser. No. 60/157,247, filed October 1, 1999;

(5) provisional application Ser. No. 60/167,824, filed November 29, 1999;

(6) provisional application Ser. No. 60/182,711, filed February 15, 2000;

all of which are incorporated by reference herein.

FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260; the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260; the nucleotide sequence of the full-length protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(bb) the nucleotide sequence of the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325; the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325; the nucleotide sequence of the full-length protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having

biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322; the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322; the nucleotide sequence of the full-length protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629; the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629; the nucleotide sequence of the full-length protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(bb) the nucleotide sequence of the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298; the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298; the nucleotide sequence of the full-length protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607; the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607; the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477; the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477; the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(ab) the nucleotide sequence of the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 47 to amino acid 56 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624; the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 89 to amino acid 98 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090; the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090; the nucleotide sequence of the full-length protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ab) the nucleotide sequence of the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(bb) the nucleotide sequence of the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275; the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275; the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(ab) the nucleotide sequence of the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340; the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340; the nucleotide sequence of the full-length protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(ab) the nucleotide sequence of the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:22.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111; the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111; the nucleotide sequence of the full-length protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114; or the nucleotide sequence of a mature protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114.

In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 175 to amino acid 184 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513; the nucleotide sequence of the full-length protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115; or the nucleotide sequence of a mature protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(ab) the nucleotide sequence of the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(bb) the nucleotide sequence of the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345; the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345; the nucleotide sequence of the full-length protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236; the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236; the nucleotide sequence of the full-length protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(bb) the nucleotide sequence of the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884; the nucleotide sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884; the nucleotide sequence of the full-length protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:32;

(b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 120 to amino acid 129 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206; the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206; the nucleotide sequence of the full-length protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-

362; or the nucleotide sequence of a mature protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253; the nucleotide sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253; the nucleotide sequence of the full-length protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vb30_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(ab) the nucleotide sequence of the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424; the nucleotide sequence of the full-length

protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:38;

(b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261; the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261; the nucleotide sequence of the full-length protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(ab) the nucleotide sequence of the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(bb) the nucleotide sequence of the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261. Also preferably the polynucleotide isolated according to the above

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038; the nucleotide sequence of the full-length protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 239 to amino acid 248 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 239 to amino acid 248 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363; the nucleotide sequence of the full-length protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(bb) the nucleotide sequence of the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707; the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707; the nucleotide sequence of the full-length protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(ab) the nucleotide sequence of the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5' end

of said sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:46;

(b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 107 to amino acid 116 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295; the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295; the nucleotide sequence of the full-length protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by

the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 74 to nucleotide 295. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:48;

(b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383; the nucleotide sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ab) the nucleotide sequence of the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(bb) the nucleotide sequence of the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383, and extending contiguously from a

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:50;

(b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739; the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739; the nucleotide sequence of the full-length protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362; or the nucleotide sequence of a mature protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 254 to amino acid 263 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(ab) the nucleotide sequence of the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

(b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 254 to amino acid 263 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835; the nucleotide sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835; the nucleotide sequence of the full-length protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:53 from nucleotide 632 to nucleotide 835, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329; the nucleotide sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329; the nucleotide sequence of the full-length protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(bb) the nucleotide sequence of the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:57.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439; the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439; the nucleotide sequence of the full-length protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(ab) the nucleotide sequence of the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bb) the nucleotide sequence of the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 30 to amino acid 39 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341; the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341; the nucleotide sequence of the full-length protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(ab) the nucleotide sequence of the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(bb) the nucleotide sequence of the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599; the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599; the nucleotide sequence of the full-length protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451; the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451; the nucleotide sequence of the full-length protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-

366; or the nucleotide sequence of a mature protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:64;

(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231; the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231; the nucleotide sequence of the full-length protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(ab) the nucleotide sequence of the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:66;

(b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 28 to amino acid 37 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736; the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736; the nucleotide sequence of the full-length protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(ab) the nucleotide sequence of the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from

nucleotide 83 to nucleotide 736, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:68;

(b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 114 to amino acid 123 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399; the nucleotide sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399; the nucleotide sequence of the full-length protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(ab) the nucleotide sequence of the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(bb) the nucleotide sequence of the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 211 to amino acid 220 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595; the nucleotide sequence of the full-length protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 232 to amino acid 241 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311; the nucleotide sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311; the nucleotide sequence of the full-length protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(bb) the nucleotide sequence of the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:74;

(b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798; the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798; the nucleotide sequence of the full-length protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(ab) the nucleotide sequence of the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:76;

(b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 116 to amino acid 125 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307; the nucleotide sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307; the nucleotide sequence of the full-length protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366; or the nucleotide sequence of a mature protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(ab) the nucleotide sequence of the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 26 to nucleotide 307. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 101 to nucleotide 307.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:78;

(b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228; the nucleotide sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228; the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:79 from nucleotide 94 to nucleotide 228, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427; the nucleotide sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427; the nucleotide sequence of the full-length protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82

having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ab) the nucleotide sequence of the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bb) the nucleotide sequence of the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:82;

(b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475; the nucleotide sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475; the nucleotide sequence of the full-length protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

(ab) the nucleotide sequence of the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83, but excluding the poly(A) tail at the 3' end of SEQ ID NO:83; and

(bb) the nucleotide sequence of the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:83. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:84;

(b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:85.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323; the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323; the nucleotide sequence of the full-length protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of

SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:86;

(b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452; the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(ab) the nucleotide sequence of the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from

nucleotide 72 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;

(b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378; the nucleotide sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378; the nucleotide sequence of the full-length protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(bb) the nucleotide sequence of the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:90;

(b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 25 to amino acid 34 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718; the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718; the nucleotide sequence of the full-length protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:91 from nucleotide 173 to nucleotide 718, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:92;

(b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762; the nucleotide sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide

encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(bb) the nucleotide sequence of the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:94;

(b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792; the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792; the nucleotide sequence of the full-length protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(bb) the nucleotide sequence of the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

(b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 109 to amino acid 118 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:97.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315; the nucleotide sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315; the nucleotide sequence of the full-length protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368. In other preferred

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and

(ab) the nucleotide sequence of the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and

(bb) the nucleotide sequence of the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:98;

(b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:99.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699; the nucleotide sequence of the full-length protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368; or the nucleotide sequence of a mature protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(ab) the nucleotide sequence of the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bb) the nucleotide sequence of the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:100;

(b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and

(c) the amino acid sequence encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 100 to amino acid 109 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:101.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394; the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394; the nucleotide sequence of the full-length protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID

NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

(ab) the nucleotide sequence of the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

(bb) the nucleotide sequence of the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:102;

(b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 32 to amino acid 41 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198; the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198; the nucleotide sequence of the full-length protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(ab) the nucleotide sequence of the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(bb) the nucleotide sequence of the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:103 from nucleotide 85 to nucleotide 198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:104;

(b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552; the nucleotide sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552; the nucleotide sequence of the full-length protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 210 to amino acid 219 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320; the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320; the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(ab) the nucleotide sequence of the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(bb) the nucleotide sequence of the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:108;

(b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255; the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255; the nucleotide sequence of the full-length protein coding sequence of clone vo32_1 deposited with the ATCC under accession

number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(bb) the nucleotide sequence of the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:110;

(b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 198 to amino acid 207 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276; the nucleotide sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276; the nucleotide sequence of the full-length protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:112;

(b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 194 to amino acid 203 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429; the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429; the nucleotide sequence of the full-length protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(ab) the nucleotide sequence of the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(bb) the nucleotide sequence of the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:114;

(b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113; the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113; the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID

NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and

(ab) the nucleotide sequence of the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and

(bb) the nucleotide sequence of the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

(b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 174 to amino acid 183 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:118;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207; the nucleotide sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207; the nucleotide sequence of the full-length protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075; or the nucleotide sequence of a mature protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

(ab) the nucleotide sequence of the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

(bb) the nucleotide sequence of the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:117 from nucleotide 103 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

(a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and

(b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g. , receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "vc62_1"

A polynucleotide of the present invention has been identified as clone "vc62_1". vc62_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc62_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc62_1 protein").

The nucleotide sequence of vc62_1 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc62_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 3 to 15 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc62_1 protein. If the 'G' residue at position 254 of SEQ ID NO:1 were deleted, another potential vc62_1 reading frame and predicted amino acid sequence that would then be encoded by nucleotides 27 to 365 of SEQ ID NO:1 is reported in SEQ ID NO:169.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc62_1 should be approximately 4221 bp.

The nucleotide sequence disclosed herein for vc62_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc62_1 demonstrated at least some similarity with sequences identified as AA580489 (nn22a10.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE 1084602, mRNA sequence), AF047042 (Homo sapiens citrate synthase mRNA, complete cds), and T04200 (Sugar beet citrate synthase cDNA; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc62_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc62_1 protein demonstrated at least some similarity to sequences identified as AF047042 (citrate synthase [Homo sapiens]) and R82839 (Sugar beet citrate synthase). Based upon sequence similarity, vc62_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vp10_1"

A polynucleotide of the present invention has been identified as clone "vp10_1". vp10_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp10_1 protein").

The nucleotide sequence of vp10_1 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 19 to 31 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp10_1 protein. If another 'G' residue were inserted in SEQ ID NO:3 after the 'G' residue at position 868, another potential vp10_1 reading frame and predicted amino acid sequence that would be encoded by what would then be nucleotides 6 to 968 of SEQ ID NO:3 is reported in SEQ ID NO:170.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp10_1 should be approximately 1401 bp.

The nucleotide sequence disclosed herein for vp10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp10_1 demonstrated at least some similarity with sequences identified as AA733074 (zg79d07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 399565 3' similar to WP:C15H9.5 CE06834; mRNA sequence). The predicted amino acid sequence disclosed herein for vp10_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp10_1 protein demonstrated at least some similarity to the sequence identified as U56965 (unknown protein [Caenorhabditis elegans]). Based upon sequence similarity, vp10_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vp10_1 protein sequence centered around amino acid 270 of SEQ ID NO:4.

Clone "vp11_1"

A polynucleotide of the present invention has been identified as clone "vp11_1". vp11_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp11_1 protein").

The nucleotide sequence of vp11_1 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 5 to 17 of SEQ ID NO:6 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp11_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp11_1 should be approximately 1329 bp.

The nucleotide sequence disclosed herein for vp11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "vp13_1"

A polynucleotide of the present invention has been identified as clone "vp13_1". vp13_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp13_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp13_1 protein").

The nucleotide sequence of vp13_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8. Amino acids 13 to 25 of SEQ ID NO:8 are a predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp13_1 protein.

Other potential vp13_1 reading frames and predicted amino acid sequences are encoded by nucleotides 151 to 267 of SEQ ID NO:7, with the encoded amino acid sequence reported in SEQ ID NO:171, and by nucleotides 209 to 787 of SEQ ID NO:7, with the encoded amino acid sequence reported in SEQ ID NO:172. Amino acids 1 to 13 of SEQ ID NO:172 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:172. The protein of SEQ ID NO:172 also demonstrates significant homology to the human Notch protein, Delta proteins from various species, and other EGF-repeat-containing transmembrane proteins. A deletion or insertion causing a frame-shift in the nucleotide sequence of SEQ ID NO:7 in the region approximately between nucleotides 208 and 267 of SEQ ID NO:7 could join the reading frames of SEQ ID NO:171 and SEQ ID NO:172 into a single reading frame encoding an EGF-repeat-containing protein. Further, the region approximately between nucleotides 605 and 850 may be an alternatively spliced exon.

If the 'A' residue at position 423 of SEQ ID NO:7 were deleted, another potential vp13_1 reading frame and predicted amino acid sequence that would be encoded by what would then be nucleotides 288 to 503 of SEQ ID NO:7 is reported in SEQ ID NO:173.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp13_1 should be approximately 1048 bp.

The nucleotide sequence disclosed herein for vp13_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp13_1 demonstrated at least some similarity with sequences identified as AA190865 (zp85b02.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 626955 3' similar to TR G1336628 G1336628 EGF REPEAT TRANSMEMBRANE PROTEIN; mRNA sequence), and U57368 (Mus musculus EGF repeat transmembrane protein mRNA, complete cds). The predicted amino acid sequence disclosed herein for vp13_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp13_1 protein demonstrated at least

some similarity to sequences identified as AC004663 (Notch 3 [Homo sapiens]), R28960 (Delta D11), and U57368 (EGF repeat transmembrane protein [Mus musculus]). Based upon sequence similarity, vp13_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vp13_1 protein sequence centered around amino acid 56 of SEQ ID NO:8.

Clone "vp16_1"

A polynucleotide of the present invention has been identified as clone "vp16_1". vp16_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp16_1 protein").

The nucleotide sequence of vp16_1 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 34 to 46 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp16_1 protein. Another potential vp16_1 reading frame and predicted amino acid sequence is encoded by basepairs 1621 to 1839 of SEQ ID NO:9 and is reported in SEQ ID NO:174.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp16_1 should be approximately 2105 bp.

The nucleotide sequence disclosed herein for vp16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp16_1 demonstrated at least some similarity with sequences identified as AA523851 (ng31e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:936408, mRNA sequence). Based upon sequence similarity, vp16_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vp16_1 protein

sequence, one centered around amino acid 36 and another around amino acid 69 of SEQ ID NO:10. The nucleotide sequence of vp16_1 indicates that it may contain an Alu repetitive element.

Clone "vp21_1"

A polynucleotide of the present invention has been identified as clone "vp21_1". vp21_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp21_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp21_1 protein").

The nucleotide sequence of vp21_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 62 to 74 of SEQ ID NO:12 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp21_1 protein. Another potential vp21_1 reading frame and predicted amino acid sequence encoded by basepairs 598 to 831 of SEQ ID NO:11 is reported in SEQ ID NO:175. Amino acids 1 to 6 of SEQ ID NO:175 and amino acids 41 to 43 of SEQ ID NO:175 are predicted leader/signal sequences, with the predicted mature amino acid sequences beginning at amino acid 7 or at amino acid 44, respectively.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp21_1 should be approximately 1538 bp.

The nucleotide sequence disclosed herein for vp21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp21_1 demonstrated at least some similarity with sequences identified as AC004076 (Homo sapiens chromosome 19, cosmid R30217, complete sequence). The predicted amino acid sequence disclosed herein for vp21_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp21_1 protein demonstrated at least some similarity to

sequences identified as AC003682 (Zinc finger protein F18547_1 [Homo sapiens]) and W19106 (Tat pheromone receptor VN5). Based upon sequence similarity, vp21_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts potential transmembrane domains within the predicted vp21_1 protein sequences, one centered around amino acid 70 of SEQ ID NO:12, and one centered around amino acid 17 of SEQ ID NO:175.

Clone "vp22_1"

A polynucleotide of the present invention has been identified as clone "vp22_1". vp22_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp22_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp22_1 protein").

The nucleotide sequence of vp22_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp22_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 13 to 25 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp22_1 protein. Another potential vp22_1 reading frame and predicted amino acid sequence encoded by basepairs 408 to 1154 of SEQ ID NO:13 is reported in SEQ ID NO:176. Amino acids 40 to 52 of SEQ ID NO:176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 53. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:176. A frameshift within the nucleotide sequence of SEQ ID NO:13 approximately between nucleotides 163 and 477 could join the openreading frames of SEQ ID NO:14 and SEQ ID NO:176.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp22_1 should be approximately 1718 bp.

The nucleotide sequence disclosed herein for vp22_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp22_1 demonstrated at least some similarity with sequences identified as AA526186 (ni94h03.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:984533, mRNA sequence), AA570505 (nk64h01.s1 NCI_CGAP_Sch1 Homo sapiens cDNA clone IMAGE 1018321, mRNA sequence), AB006085 (Danio rerio mRNA for MINDIN2, complete cds), and T78360 (Human neuronal attachment factor-1 DNA; standard; DNA). The predicted amino acid sequence disclosed herein for vp22_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vp22_1 protein demonstrated at least some similarity to sequences identified as AB006085 (MINDIN2 [Danio rerio]) and W23663 (Human neuronal attachment factor-1). Based upon sequence similarity, vp22_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq2_1"

A polynucleotide of the present invention has been identified as clone "vq2_1". vq2_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq2_1 protein").

The nucleotide sequence of vq2_1 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16. Amino acids 4 to 16 of SEQ ID NO:16 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq2_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq2_1 should be approximately 896 bp.

The nucleotide sequence disclosed herein for vq2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. vq2_1 demonstrated at least some similarity with sequences identified as AI203981 (qe76h05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744953 3', mRNA sequence) and T97082 (Human haematopoietic-specific protein (HSP) DNA; standard; DNA). The predicted amino acid sequence disclosed herein for vq2_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq2_1 protein demonstrated at least some similarity to the sequence identified as W35904 (Human haematopoietic-specific protein (HSP)). Based upon sequence similarity, vq2_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq3_1"

A polynucleotide of the present invention has been identified as clone "vq3_1". vq3_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq3_1 protein").

The nucleotide sequence of vq3_1 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 11 to 23 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq3_1 should be approximately 1490 bp.

The nucleotide sequence disclosed herein for vq3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the database. The nucleotide sequence of vq3_1 indicates that it may contain an Alu repetitive element.

Clone "vq5_1"

A polynucleotide of the present invention has been identified as clone "vq5_1". vq5_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq5_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq5_1 protein").

The nucleotide sequence of vq5_1 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq5_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 9 to 21 of SEQ ID NO:20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq5_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq5_1 should be approximately 2207 bp.

The nucleotide sequence disclosed herein for vq5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq5_1 demonstrated at least some similarity with sequences identified as AQ036276 (CIT-HSP-2331M15.TF CIT-HSP Homo sapiens genomic clone 2331M15, genomic survey sequence) and T24918 (Human gene signature HUMGS07027; standard; cDNA to mRNAP). Based upon sequence similarity, vq5_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts that the signal sequence at residue 22 of SEQ ID NO:20 is also a potential transmembrane domain.

Clone "vq6_1"

A polynucleotide of the present invention has been identified as clone "vq6_1". vq6_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq6_1 protein").

The nucleotide sequence of vq6_1 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 6 to 18 of SEQ ID NO:22 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq6_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq6_1 should be approximately 1875 bp.

The nucleotide sequence disclosed herein for vq6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq6_1 demonstrated at least some similarity with sequences identified as AA729043 (nw22d09.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241201 similar to contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, vq6_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vq6_1 protein sequence centered around amino acid 37 of SEQ ID NO:22. The nucleotide sequence of vq6_1 indicates that it may contain an Alu repetitive element.

Clone "vr1_1"

A polynucleotide of the present invention has been identified as clone "vr1_1". vr1_1 was isolated from a human adult muscle cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vr1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vr1_1 protein").

The nucleotide sequence of vr1_1 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vr1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 34 to 46 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino

acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vr1_1 protein. The region of SEQ ID NO:23 approximately between nucleotides 1931 and 1977 of SEQ ID NO:23 may be an alternatively spliced exon.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vr1_1 should be approximately 1512 bp.

The nucleotide sequence disclosed herein for vr1_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vr1_1 demonstrated at least some similarity with sequences identified as AL031602 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9; HTGS phase 1), I64695 (Sequence 1 from patent US 5665588), and T35233 (Natural killer lytic associated protein cDNA; standard; cDNA). The predicted amino acid sequence disclosed herein for vr1_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vr1_1 protein demonstrated at least some similarity to sequences identified as R99256 (Natural killer lytic associated protein), and X71642 (GEG-154 gene product [Mus musculus]). Based upon sequence similarity, vr1_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vr1_1 protein sequence centered around amino acid 150 of SEQ ID NO:24.

Clone "vc63_1"

A polynucleotide of the present invention has been identified as clone "vc63_1". vc63_1 was isolated from a human fetal brain cDNA library and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc63_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "vc63_1 protein").

The nucleotide sequence of vc63_1 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc63_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Another potential

vc63_1 reading frame and predicted amino acid sequence encoded by basepairs 528 to 1100 of SEQ ID NO:25 is reported in SEQ ID NO:177. Amino acids 140 to 152 of SEQ ID NO:177 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 153. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:177.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc63_1 should be approximately 2397 bp.

The nucleotide sequence disclosed herein for vc63_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc63_1 demonstrated at least some similarity with sequences identified as N66555 (yy69b07.s1 Homo sapiens cDNA clone 278773 3') and T21367 (Human gene signature HUMGS02731; standard; cDNA to mRNA). The predicted amino acid sequence disclosed herein for vc63_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc63_1 protein demonstrated at least some similarity to the sequence identified as Z36948 (D2089.2 [Caenorhabditis elegans]). Based upon sequence similarity, vc63_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO:177, centered around amino acid 153 of SEQ ID NO:177.

Clone "vb25_1"

A polynucleotide of the present invention has been identified as clone "vb25_1". vb25_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb25_1 protein").

The nucleotide sequence of vb25_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28. Amino acids 5 to 17

of SEQ ID NO:28 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb25_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb25_1 should be approximately 1677 bp.

The nucleotide sequence disclosed herein for vb25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb25_1 demonstrated at least some similarity with sequences identified as Z73429 (Human DNA sequence from cosmid cN32F9 on chromosome 22q11.2-qter Contains CpG island). Based upon sequence similarity, vb25_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vb25_1 indicates that it may contain one or more of the following repetitive elements: AC simple repeat, AG simple repeat, ALU, MIR.

Clone "vb27_1"

A polynucleotide of the present invention has been identified as clone "vb27_1". vb27_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb27_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb27_1 protein").

The nucleotide sequence of vb27_1 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb27_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 14 to 26 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb27_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb27_1 should be approximately 3456 bp.

The nucleotide sequence disclosed herein for vb27_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb27_1 demonstrated at least some similarity with sequences identified as AC005035 (Homo sapiens BAC clone NH0353P23 from 2, complete sequence) and H73579 (yu29f09.r1 Homo sapiens cDNA clone 235241 5'). Based upon sequence similarity, vb27_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vb27_1 indicates that it may contain one or mor of the following repetitive elements: ALU, Mer3.

Clone "vb28_1"

A polynucleotide of the present invention has been identified as clone "vb28_1". vb28_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb28_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb28_1 protein").

The nucleotide sequence of vb28_1 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb28_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 4 to 16 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb28_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb28_1 should be approximately 3008 bp.

The nucleotide sequence disclosed herein for vb28_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb28_1 demonstrated at least some similarity with sequences identified as AA046671 (zf12d09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:376721 5' similar to PIR:A38745 A38745 cell adhesion molecule CD44 precursor - rat; mRNA sequence) and V22687 (DNA encoding a CD44-like protein). The predicted amino acid sequence disclosed herein for vb28_1 was searched against the

GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vb28_1 protein demonstrated at least some similarity to sequences identified as W56249 (Amino acid sequence of a CD44-like protein) and X66081 (CD44 [Mus musculus]). Based upon sequence similarity, vb28_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vb29_1"

A polynucleotide of the present invention has been identified as clone "vb29_1". vb29_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb29_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb29_1 protein").

The nucleotide sequence of vb29_1 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb29_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 11 to 23 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb29_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb29_1 should be approximately 2970 bp.

The nucleotide sequence disclosed herein for vb29_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vb29_1 demonstrated at least some similarity with sequences identified as AA084068 (zn16d12.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547607 5', mRNA sequence) and AQ418918 (RPCI-11-185K12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185K12, genomic survey sequence). Based upon sequence similarity, vb29_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vb29_1 protein sequence centered

around amino acid 41 of SEQ ID NO:34. The nucleotide sequence of vb29_1 indicates that it may contain an Alu repetitive element.

Clone "vb30_1"

A polynucleotide of the present invention has been identified as clone "vb30_1". vb30_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vb30_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vb30_1 protein").

The nucleotide sequence of vb30_1 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vb30_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. Amino acids 15 to 27 of SEQ ID NO:36 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vb30_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vb30_1 should be approximately 3325 bp.

The nucleotide sequence disclosed herein for vb30_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. The nucleotide sequence of vb30_1 indicates that it may contain an Alu repetitive element.

Clone "vc67_1"

A polynucleotide of the present invention has been identified as clone "vc67_1". vc67_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc67_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc67_1 protein").

The nucleotide sequence of vc67_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vc67_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Another potential vc67_1 reading frame and predicted amino acid sequence encoded by basepairs 3 to 242 of SEQ ID NO:37 is reported in SEQ ID NO:178.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc67_1 should be approximately 2305 bp.

The nucleotide sequence disclosed herein for vc67_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc67_1 demonstrated at least some similarity with sequences identified as T23222 (Human gene signature HUMGS05018), W87297 (zh67h03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE 417173 3', mRNA sequence), and Z97201 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE). The predicted amino acid sequence disclosed herein for vc67_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc67_1 protein demonstrated at least some similarity to sequences identified as W69427 (Human secreted protein bk291_3) and Z68751 (Similarity to Yeast hypothetical protein YKK0 (SW YKK0_YEAST); cDNA EST EMBL C12578 comes from this gene; cDNA EST yk329g12.5 comes from this gene; cDNA EST yk415). Based upon sequence similarity, vc67_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vc67_1 protein sequence of SEQ ID NO:38, one centered around amino acid 58 and another around amino acid 85 of SEQ ID NO:38.

Clone "vf4_1"

A polynucleotide of the present invention has been identified as clone "vf4_1". vf4_1 was isolated from a human adult heart cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vf4_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vf4_1 protein").

The nucleotide sequence of vf4_1 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vf4_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40. Amino acids 5 to 17 of SEQ ID NO:40 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vf4_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vf4_1 should be approximately 972 bp.

The nucleotide sequence disclosed herein for vf4_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vf4_1 demonstrated at least some similarity with sequences identified as AA813690 (ai71a09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376248 3', mRNA sequence) and V86544 (EST clone AZ285). Based upon sequence similarity, vf4_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vg3_1"

A polynucleotide of the present invention has been identified as clone "vg3_1". vg3_1 was isolated from a human adult brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vg3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vg3_1 protein").

The nucleotide sequence of vg3_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vg3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 13 to 25 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vg3_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vg3_1 should be approximately 3667 bp.

The nucleotide sequence disclosed herein for vg3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vg3_1 demonstrated at least some similarity with sequences identified as AI283122 (qm51h10.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE 1892323 3', mRNA sequence). The predicted amino acid sequence disclosed herein for vg3_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vg3_1 protein demonstrated at least some similarity to sequences identified as U53155 (ZC513.5 [Caenorhabditis elegans]). Based upon sequence similarity, vg3_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts the following transmembrane domains within the vg3_1 protein sequence: four certain transmembrane domains centered around amino acids 78, 133, 156, and 298 of SEQ ID NO:42, respectively; four strongly putative transmembrane domains centered around amino acids 105, 189, 221, and 354 of SEQ ID NO:42, respectively; and six possible transmembrane domains centered around amino acids 262, 272, 322, 367, 432, and 460 of SEQ ID NO:42, respectively. Motifs analysis detected a Crystallins beta and gamma 'Greek key' motif signature around amino acid 52 of SEQ ID NO:42. The nucleotide sequence of vg3_1 indicates that it may contain an Alu repetitive element.

Clone "vo2_1"

A polynucleotide of the present invention has been identified as clone "vo2_1". vo2_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo2_1 protein").

The nucleotide sequence of vo2_1 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

Another potential vo2_1 reading frame and predicted amino acid sequence encoded by basepairs 95 to 280 of SEQ ID NO:43 is reported in SEQ ID NO:179. Amino acids 9 to 21 of SEQ ID NO:179 are a predicted leader/signal sequence, with the predicted mature

amino acid sequence of the encoded protein. vo3_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo3_1 protein").

The nucleotide sequence of vo3_1 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo3_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 107 to 119 of SEQ ID NO:46 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 120. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo3_1 protein.

If a "C" residue were to be deleted from the nucleotide sequence of SEQ ID NO:45 at either position 917 or position 918, another potential vo3_1 reading frame and predicted amino acid sequence encoded by what would then be basepairs 697 to 1377 of SEQ ID NO:45 is reported in SEQ ID NO:182. Amino acids 62 to 74 of SEQ ID NO:182 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 75. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:182.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo3_1 should be approximately 1592 bp.

The nucleotide sequence disclosed herein for vo3_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo3_1 demonstrated at least some similarity with sequences identified as AA530997 (nj07a06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:985618 3', mRNA sequence), AA683481 (zl55b03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:505805 3', mRNA sequence), D88158 (Pig mRNA for cytochrome b561, complete cds), and V84516 (Human secreted protein gene 106 clone HTOEY16). The predicted amino acid sequence disclosed herein for vo3_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo3_1 protein demonstrated at least some similarity to sequences identified as U06715 (HCYTO B561 [Homo sapiens]) and W89024 (Polypeptide fragment encoded by gene 156). Based upon sequence similarity, vo3_1

proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the vo3_1 protein sequence, centered around amino acids 35, 75, 113, 146, and 191 of SEQ ID NO:46, respectively.

Clone "vo5_1"

A polynucleotide of the present invention has been identified as clone "vo5_1". vo5_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo5_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo5_1 protein").

The nucleotide sequence of vo5_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo5_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 8 to 20 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo5_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo5_1 should be approximately 2487 bp.

The nucleotide sequence disclosed herein for vo5_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo5_1 demonstrated at least some similarity with sequences identified as AA868551 (ak43f09.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1408745 3', mRNA sequence) and AC005500 (complete sequence [Homo sapiens Chromosome 22q11 PAC Clone p52f6 In DGCR Region]). Based upon sequence similarity, vo5_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo5_1 indicates that it may contain an Alu repetitive element.

Clone "vo6_1"

A polynucleotide of the present invention has been identified as clone "vo6_1". vo6_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo6_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo6_1 protein").

The nucleotide sequence of vo6_1 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo6_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50. Amino acids 77 to 89 of SEQ ID NO:50 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 90. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo6_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo6_1 should be approximately 1272 bp.

The nucleotide sequence disclosed herein for vo6_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols.. vo6_1 demonstrated at least some similarity with sequences identified as AL020989 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 192P9; HTGS phase 1), T34592 (NTII-11 nerve protein coding sequence), and U13617 (Rattus norvegicus Sprague-Dawley plasmolipin mRNA, complete cds). The predicted amino acid sequence disclosed herein for vo6_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo6_1 protein demonstrated at least some similarity to sequences identified as R99799 (NTII-11 nerve protein, facilitates regeneration of nerve cells) and U13617 (plasmolipin [Rattus norvegicus]). Plasmolipin is an 18-kDa proteolipid protein found in kidney and brain, where it is restricted to the apical surface of tubular epithelial cells and to mammalian myelinated tracts, respectively; addition of plasmolipin to lipid bilayers induces the formation of ion channels, which are voltage-dependent and K(+)-selective. (*See* Fischer and Sapirstein , 1994, *J. Biol. Chem.* **269(40)**: 24912-24919, which is incorporated by reference herein). Based upon sequence similarity, vo6_1 proteins and

each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the vo6_1 protein sequence, centered around amino acids 14, 42, and 90 of SEQ ID NO:50, respectively.

Clone "vo9_1"

A polynucleotide of the present invention has been identified as clone "vo9_1". vo9_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo9_1 protein").

The nucleotide sequence of vo9_1 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 22 to 34 of SEQ ID NO: are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo9_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo9_1 should be approximately 3331 bp.

The nucleotide sequence disclosed herein for vo9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo9_1 demonstrated at least some similarity with sequences identified as AA936961 (oo65f04.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE 1571071 3', mRNA sequence), AF010496 9Rhodobacter capsulatus strain SB1003, partial genome), AL035661 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 568C11, WORKING DRAFT SEQUENCE), and Q24673 (facA gene). The predicted amino acid sequence disclosed herein for vo9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo9_1 protein demonstrated at least some similarity to sequences identified as R23968 (facA gene product) and Y15417 (acetate--CoA ligase

[Coprinus cinereus]). Based upon sequence similarity, vo9_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo11_1"

A polynucleotide of the present invention has been identified as clone "vo11_1". vo11_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo11_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo11_1 protein").

The nucleotide sequence of vo11_1 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo11_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 52 to 64 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 65.

Another potential vo11_1 reading frame and predicted amino acid sequence, encoded by basepairs 18 to 308 of SEQ ID NO:53, is reported in SEQ ID NO:183. Amino acids 10 to 22 of SEQ ID NO:183 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:183.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo11_1 should be approximately 1509 bp.

The nucleotide sequence disclosed herein for vo11_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo11_1 demonstrated at least some similarity with sequences identified as D83866 (similar to none, mRNA sequence). Based upon sequence similarity, vo11_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo12_1"

A polynucleotide of the present invention has been identified as clone "vo12_1". vo12_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo12_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo12_1 protein").

The nucleotide sequence of vo12_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo12_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 4 to 16 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17.

Another potential vo12_1 reading frame and predicted amino acid sequence, encoded by basepairs 107 to 310 of SEQ ID NO:55, is reported in SEQ ID NO:184. Amino acids 14 to 26 and amino acids 18 to 30 of SEQ ID NO:184 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 27 or at amino acid 31, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:184.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo12_1 should be approximately 986 bp.

The nucleotide sequence disclosed herein for vo12_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo12_1 demonstrated at least some similarity with sequences identified as AA444152 (zv51g06.r1 Soares testis NHT Homo sapiens cDNA clone 757210 5', mRNA sequence). Based upon sequence similarity, vo12_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo12_1 protein sequence centered around amino acid 51 of SEQ ID NO:56.

Clone "vo13_1"

A polynucleotide of the present invention has been identified as clone "vo13_1". vo13_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. The vo13_1 clone includes coding sequence of a secreted protein (also referred to herein as "vo13_1 protein").

The nucleotide sequence of vo13_1 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58. Amino acids 8 to 20 of SEQ ID NO:58 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo13_1 should be approximately 1073 bp.

The nucleotide sequence disclosed herein for vo13_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo13_1 demonstrated at least some similarity with sequences identified as AA988298 (os32a02.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1607018 3', mRNA sequence) and V69614 (Human secreted protein gene 4 clone HE8ND56). The predicted amino acid sequence disclosed herein for vo13_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo13_1 protein demonstrated at least some similarity to sequences identified as W83934 (Human secreted protein from gene 4 clone HE8ND56). Based upon sequence similarity, vo13_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo13_1 protein sequence centered around amino acid 50 of SEQ ID NO:58.

Clone "vo14_1"

A polynucleotide of the present invention has been identified as clone "vo14_1". vo14_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vo14_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo14_1 protein").

The nucleotide sequence of vo14_1 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo14_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60. Amino acids 14 to 26 of SEQ ID NO:60 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo14_1 should be approximately 1605 bp.

The nucleotide sequence disclosed herein for vo14_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant hits were found in the databases. Based upon sequence similarity, vo14_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo14_1 indicates that it may contain one or more of the following repetitive elements: Alu, TAAAA repeat.

Clone "vo15_1"

A polynucleotide of the present invention has been identified as clone "vo15_1". vo15_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo15_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo15_1 protein").

The nucleotide sequence of vo15_1 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo15_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino acids 13 to 25 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

If a nucleotide were deleted between nucleotide 458 and nucleotide 460 of SEQ ID NO:61, another potential vo15_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 90 to 515 of SEQ ID NO:61, is reported in SEQ

ID NO:185. Amino acids 16 to 28 and amino acids 13 to 25 of SEQ ID NO:185 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 29 or at amino acid 26, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:185.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo15_1 should be approximately 2842 bp.

The nucleotide sequence disclosed herein for vo15_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo15_1 demonstrated at least some similarity with sequences identified as AI096756 (qb46e10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE 1703178 3', mRNA sequence). Based upon sequence similarity, vo15_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo15_1 protein sequence centered around amino acid 126 of SEQ ID NO:62. The nucleotide sequence of vo15_1 indicates that it may contain one ore more repeat sequences.

Clone "vo16_1"

A polynucleotide of the present invention has been identified as clone "vo16_1". vo16_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo16_1 protein").

The nucleotide sequence of vo16_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 51 to 63 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 64. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo16_1 protein.

If an "A" or "G" nucleotide were inserted between nucleotides 102 and 103of SEQ ID NO:63 and an additional "A" residue inserted between nucleotides 271 and 273 of SEQ ID NO:63, another potential vo16_1 reading frame and predicted amino acid sequence, encoded by what would then be basepairs 6 to 338 of SEQ ID NO:63, is reported in SEQ ID NO:. Amino acids 5 to 17 and amino acids 4 to 16 of SEQ ID NO:186 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 18 or at amino acid 17, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:186.

Another potential vo16_1 reading frame and predicted amino acid sequence, encoded by basepairs 846 to 1061 of SEQ ID NO:63, is reported in SEQ ID NO:187. Amino acids 12 to 24 and amino acids 11 to 23 of SEQ ID NO:187 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 25 or at amino acid 24, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:187.

Nucleotides 1 to 133 of SEQ ID NO:63 are nearly identical to nucleotides 862 to 994 of SEQ ID NO:63, resulting in amino acids 1 to 33 of SEQ ID NO:186 being identical to amino acids 8 to 40 of SEQ ID NO:187.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo16_1 should be approximately 2113 bp.

The nucleotide sequence disclosed herein for vo16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo16_1 demonstrated at least some similarity with sequences identified as R79825 (yi89a06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146386 3', mRNA sequence). Based upon sequence similarity, vo16_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo16_1 protein sequence centered around amino acid 64 of SEQ ID NO:64. The nucleotide sequence of vo16_1 indicates that it may contain an Alu repeat region.

Clone "vo18_1"

A polynucleotide of the present invention has been identified as clone "vo18_1". vo18_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo18_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo18_1 protein").

The nucleotide sequence of vo18_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo18_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 10 to 22 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo18_1 should be approximately 624 bp.

The nucleotide sequence disclosed herein for vo18_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo18_1 demonstrated at least some similarity with sequences identified as AI198956 (qf66h01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 1755025 3', mRNA sequence). Based upon sequence similarity, vo18_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo19_1"

A polynucleotide of the present invention has been identified as clone "vo19_1". vo19_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo19_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo19_1 protein").

The nucleotide sequence of vo19_1 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo19_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 8 to 20

of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo19_1 should be approximately 1957 bp.

The nucleotide sequence disclosed herein for vo19_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo19_1 demonstrated at least some similarity with sequences identified as AI524085 (th01e09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2117032 3', mRNA sequence) and V42646 (DNA encoding a human pathogenesis-related protein designated HPRP). The predicted amino acid sequence disclosed herein for vo19_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo19_1 protein demonstrated at least some similarity to sequences identified as U16307 (glioma pathogenesis-related protein [Homo sapiens] and W63115 (A human pathogenesis-related protein designated HPRP). Based upon sequence similarity, vo19_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo22_1"

A polynucleotide of the present invention has been identified as clone "vo22_1". vo22_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo22_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo22_1 protein").

The nucleotide sequence of vo22_1 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo22_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 6 to 18 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19.

If one of the "G" nucleotides at positions 385 and 386 of SEQ ID NO:69 were deleted, and the "G" residue at position 312 of SEQ ID NO:69 changed to a "T", another potential vo22_1 reading frame and predicted amino acid sequence, encoded by what

would then be basepairs 104 to 430 of SEQ ID NO:69, is reported in SEQ ID NO:188. Amino acids 8 to 20, amino acids 7 to 19, amino acids 6 to18, and amino acids 9 to 21 of SEQ ID NO:188 are predicted leader/signal sequences, with the predicted mature amino acid sequence beginning at amino acid 21, or at amino acid 20, or at amino acid 19,or at amino acid 22, respectively. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:188.

Another potential vo22_1 reading frame and predicted amino acid sequence, encoded by basepairs 1150 to 1357 of SEQ ID NO:69, is reported in SEQ ID NO:189. Amino acids 3 to 15 of SEQ ID NO:189 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:189.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo22_1 should be approximately 2091 bp.

The nucleotide sequence disclosed herein for vo22_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo22_1 demonstrated at least some similarity with sequences identified as AA706247 (ah28c11.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 1240148 3', mRNA sequence) and V34194 (Human secreted protein gene 41 clone HNTME13). The predicted amino acid sequence disclosed herein for vo22_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo22_1 protein demonstrated at least some similarity to sequences identified as AF01644 (No definition line found [Caenorhabditis elegans]) and W75155 (Human secreted protein encoded by gene 41 clone HNTME13). Based upon sequence similarity, vo22_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts 9 potential transmembrane domains within the vo22_1 protein sequence, centered around amino acids 50, 120, 165, 250, 275, 309, 356, 374, and 392 of SEQ ID NO:70, respectively.

Clone "vo23_1"

A polynucleotide of the present invention has been identified as clone "vo23_1". vo23_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo23_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo23_1 protein").

The nucleotide sequence of vo23_1 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo23_1 should be approximately 2598 bp.

The nucleotide sequence disclosed herein for vo23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo23_1 demonstrated at least some similarity with sequences identified as T23658 (Human gene signature HUMGS05523), W81246 (zd85b01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347401 5', mRNA sequence), and Z84488 (Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island). Based upon sequence similarity, vo23_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the vo23_1 protein sequence, one centered around amino acid 428 and another around amino acid 472 of SEQ ID NO:72.

Clone "vo24_1"

A polynucleotide of the present invention has been identified as clone "vo24_1". vo24_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo24_1 protein").

The nucleotide sequence of vo24_1 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the vo24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 10 to 22 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo24_1 should be approximately 3484 bp.

The nucleotide sequence disclosed herein for vo24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo24_1 demonstrated at least some similarity with sequences identified as AC003117 (*** SEQUENCING IN PROGRESS *** Human chromosome 1 BAC 308G1 genomic sequence; HTGS phase 1, 3 unordered pieces), V10696 (Human 3.5 kB DNA fragment predicted to contain CH1-9a11-2 gene), and Z94054 (Human DNA sequence from PAC 125H23 on chromosome 1q24-1q25). The predicted amino acid sequence disclosed herein for vo24_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo24_1 protein demonstrated at least some similarity to sequences identified as W58774 (Human breast cancer gene CH1-9a11-2 protein fragment #1). Based upon sequence similarity, vo24_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo24_1 indicates that it may contain one or more of the following repetitive elements: Alu, Mer33.

Clone "vo25_1"

A polynucleotide of the present invention has been identified as clone "vo25_1". vo25_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo25_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo25_1 protein").

The nucleotide sequence of vo25_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo25_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 11 to 23

of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo25_1 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for vo25_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo25_1 demonstrated at least some similarity with sequences identified as AI300566 (qn56a09.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE 1902232 3' similar to WP C35D10.1 CE01190 ;, mRNA sequence), V34218 (Human secreted protein gene 65 clone HSREG44), and Z55702 (H.sapiens CpG island DNA genomic Mse1 fragment, clone 58e10, forward read cpg58e10.ft1a). The predicted amino acid sequence disclosed herein for vo25_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo25_1 protein demonstrated at least some similarity to sequences identified as U21324 (similar to S. cerevisiae hypothetical protein YKL166 [Caenorhabditis elegans]) and W57893 (Protein of clone AT340_1). Based upon sequence similarity, vo25_1 proteins and each similar protein or peptide may share at least some activity. Motifs analysis detected an ATP/GTP-binding site motif A (P-loop) centered around residue 229 of SEQ ID NO:76. The TopPredII computer program predicts a potential transmembrane domain within the vo25_1 protein sequence centered around amino acid 170 of SEQ ID NO:76.

Clone "vo26_1"

A polynucleotide of the present invention has been identified as clone "vo26_1". vo26_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo26_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo26_1 protein").

The nucleotide sequence of vo26_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo26_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78. Amino acids 13 to 25

of SEQ ID NO:78 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo26_1 should be approximately 2503 bp.

The nucleotide sequence disclosed herein for vo26_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo26_1 demonstrated at least some similarity with sequences identified as AC004707 (Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence), AI160442 (qc08g02.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE 1709042 3' similar to SW RM02_YEAST P12687 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR; mRNA sequence), and T23473 (Human gene signature HUMGS05312). The predicted amino acid sequence disclosed herein for vo26_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo26_1 protein demonstrated at least some similarity to sequences identified as L37877 (ribosomal protein L27 [Filobasidiella neoformans]). Based upon sequence similarity, vo26_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vo26_1 indicates that it may contain a Mir repeat.

Clone "vp23_1"

A polynucleotide of the present invention has been identified as clone "vp23_1". vp23_1 was isolated from a human adult prostate cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vp23_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vp23_1 protein").

The nucleotide sequence of vp23_1 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vp23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 5 to 17 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted

leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vp23_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vp23_1 should be approximately 1220 bp.

The nucleotide sequence disclosed herein for vp23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vp23_1 demonstrated at least some similarity with sequences identified as AL021578 (Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)), predicts a gene like the mouse transcription factor RBP-L). Based upon sequence similarity, vp23_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vp23_1 indicates that it may contain an Alu repetitive element.

Clone "vq7_1"

A polynucleotide of the present invention has been identified as clone "vq7_1". vq7_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq7_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq7_1 protein").

The nucleotide sequence of vq7_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq7_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 9 to 21 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq7_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq7_1 should be approximately 1326 bp.

The nucleotide sequence disclosed herein for vq7_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq7_1 demonstrated at least some similarity with sequences

identified as AA036918 (zk32e03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 484540 5', mRNA sequence). The predicted amino acid sequence disclosed herein for vq7_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq7_1 protein demonstrated at least some similarity to sequences identified as AF142780 (butyrophilin-like protein [Mus musculus]). Butyrophilin is a glycoprotein of the immunoglobulin superfamily that is secreted in association with the milk-fat-globule membrane from mammary epithelial cells (Ogg *et al.*, 1996, *Mamm. Genome* 7 (12): 900-905, which is incorporated by reference herein). Based upon sequence similarity, vq7_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vq7_1 indicates that it may contain a repetitive element.

Clone "vq8_1"

A polynucleotide of the present invention has been identified as clone "vq8_1". vq8_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq8_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq8_1 protein").

The nucleotide sequence of vq8_1 as presently determined is reported in SEQ ID NO:83, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq8_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 10 to 22 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq8_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq8_1 should be approximately 695 bp.

The nucleotide sequence disclosed herein for vq8_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq8_1 demonstrated at least some similarity with sequences identified as AA433968 (zw23f07.r1 Soares ovary tumor NbHOT Homo sapiens cDNA

clone 770149 5', mRNA sequence) and V69618 (Human secreted protein gene 8 clone HLHCM89). The predicted amino acid sequence disclosed herein for vq8_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq8_1 protein demonstrated at least some similarity to sequences identified as W83953 (Polypeptide encoded by gene 7 clone HJPDJ64). Based upon sequence similarity, vq8_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq9_1"

A polynucleotide of the present invention has been identified as clone "vq9_1". vq9_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq9_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq9_1 protein").

The nucleotide sequence of vq9_1 as presently determined is reported in SEQ ID NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq9_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 5 to 17 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq9_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq9_1 should be approximately 1218 bp.

The nucleotide sequence disclosed herein for vq9_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq9_1 demonstrated at least some similarity with sequences identified as AA769310 (nz39f03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1290173, mRNA sequence). The predicted amino acid sequence disclosed herein for vq9_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq9_1 protein demonstrated at least some similarity to sequences identified as U79260 (unknown [Homo sapiens]) and

W48351 (Human breast cancer related protein BCRB2). Based upon sequence similarity, vq9_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq10_1"

A polynucleotide of the present invention has been identified as clone "vq10_1". vq10_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq10_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq10_1 protein").

The nucleotide sequence of vq10_1 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq10_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 6 to 18 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq10_1 protein.

Another potential reading frame, encoded by nucleotides 331 to 834 of SEQ ID NO:87, is reported as the amino acid sequence of SEQ ID NO:190. Amino acids 29 to 41 of SEQ ID NO:190 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 42. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:190.

If one nucleotide was deleted from the group of nucleotides at positions 330 and 331 of SEQ ID NO:87, another potential reading frame would be created from what would then be nucleotides 18 to 836, with a predicted amino acid sequence reported as SEQ ID NO:191. Amino acids 6 to 18 of SEQ ID NO:191 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:191.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq10_1 should be approximately 1516 bp.

The nucleotide sequence disclosed herein for vq10_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq10_1 demonstrated at least some similarity with sequences identified as AA359702 (EST68843 Fetal lung II Homo sapiens cDNA 5' end similar to similar to pulmonary surfactant protein B, mRNA sequence), I08571 (Sequence 14 from Patent WO 8706588), and Q79287 (Human pulmonary surfactant protein B (SPB)). The predicted amino acid sequence disclosed herein for vq10_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq10_1 protein demonstrated at least some similarity to sequences identified as J02761 (pulmonary surfactant-associated protein SP-B [Homo sapiens]) and P70664 (6kd pulmonary surfactant protein). Pulmonary surfactant associated proteins such as SP-B promote alveolar stability by lowering the surface tension at the air-liquid interface in the peripheral air spaces. Based upon sequence similarity, vq10_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vq10_1 indicates that it may contain an Alu repetitive element.

Clone "vq13_1"

A polynucleotide of the present invention has been identified as clone "vq13_1". vq13_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq13_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq13_1 protein").

The nucleotide sequence of vq13_1 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq13_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 10 to 22 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq13_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq13_1 should be approximately 2284 bp.

The nucleotide sequence disclosed herein for vq13_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq13_1 demonstrated at least some similarity with sequences identified as AA928678 (on48e07.s1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE 1559940 3', mRNA sequence), AB023187 (Homo sapiens mRNA for KIAA0970 protein, complete cds), and T19039 (Human gene signature HUMGS00046). Based upon sequence similarity, vq13_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vq16_1"

A polynucleotide of the present invention has been identified as clone "vq16_1". vq16_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq16_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq16_1 protein").

The nucleotide sequence of vq16_1 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq16_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 34 to 46 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq16_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq16_1 should be approximately 1087 bp.

The nucleotide sequence disclosed herein for vq16_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq16_1 demonstrated at least some similarity with sequences identified as AA400700 (zu70g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743396 5' similar to WP:R05D3.2 CE00281; mRNA sequence). The predicted

amino acid sequence disclosed herein for vq16_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq16_1 protein demonstrated at least some similarity to sequences identified as AF05611 (unknown [Fugu rubripes]). Based upon sequence similarity, vq16_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the vq16_1 protein sequence, centered around amino acids 90, 134, and 174 of SEQ ID NO:92, respectively.

Clone "vq19_1"

A polynucleotide of the present invention has been identified as clone "vq19_1". vq19_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq19_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq19_1 protein").

The nucleotide sequence of vq19_1 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq19_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 11 to 23 of SEQ ID NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq19_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq19_1 should be approximately 1833 bp.

The nucleotide sequence disclosed herein for vq19_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq19_1 demonstrated at least some similarity with sequences identified as AA577696 (nn22h03.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1084661 3' similar to contains Alu repetitive element; mRNA sequence. Based upon sequence similarity, vq19_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential

transmembrane domains within the vq19_1 protein sequence centered around amino acid 214 of SEQ ID NO:94. The nucleotide sequence of vq19_1 indicates that it may contain an Alu repetitive element.

Clone "vq20_1"

A polynucleotide of the present invention has been identified as clone "vq20_1". vq20_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq20_1 protein").

The nucleotide sequence of vq20_1 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq20_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96. Amino acids 10 to 22 of SEQ ID NO:96 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 23. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq20_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq20_1 should be approximately 1275 bp.

The nucleotide sequence disclosed herein for vq20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq20_1 demonstrated at least some similarity with sequences identified as AA826249 (of11c04.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE 1420806 3' similar to TR Q13445 Q13445 PUTATIVE T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR; mRNA sequence), AI129838 (qc49h11.x1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone IMAGE:1712997 3' similar to TR:Q13445 Q13445 PUTATIVE T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR; mRNA sequence), U41805 (Mus musculus putative T1/ST2 receptor binding protein precursor mRNA, partial cds), and V17729 (Human T1 receptor-like ligand II cDNA). The predicted amino acid sequence disclosed herein for vq20_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted vq20_1 protein demonstrated at least some similarity to sequences identified as U41804 (putative T1/ST2 receptor binding protein precursor [Homo sapiens]) and W48335 (Human T1 receptor-like ligand II). T1/ST2 is a receptor-like molecule homologous to the type I interleukin-1 receptor (Gayle *et al.*, 1996, *J. Biol. Chem.* 271 (10): 5784-5789, which is incorporated by reference herein). Based upon sequence similarity, vq20_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the vq20_1 protein sequence centered around amino acid 208 of SEQ ID NO:96.

Clone "vq21_1"

A polynucleotide of the present invention has been identified as clone "vq21_1". vq21_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq21_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq21_1 protein").

The nucleotide sequence of vq21_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq21_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Amino acids 16 to 28 of SEQ ID NO:98 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 29. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq21_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq21_1 should be approximately 1230 bp.

The nucleotide sequence disclosed herein for vq21_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq21_1 demonstrated at least some similarity with sequences identified as AA149768 (zo01g05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE 566456 3' similar to contains Alu repetitive element; mRNA sequence), AC005282 (Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4

unordered pieces), T25413 (Human gene signature HUMGS07579). The predicted amino acid sequence disclosed herein for vq21_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vq21_1 protein demonstrated at least some similarity to sequences identified as U67577 (cell division protein FtsJ [Methanococcus jannaschii]). Based upon sequence similarity, vq21_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vr2_1"

A polynucleotide of the present invention has been identified as clone "vr2_1". vr2_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vr2_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vr2_1 protein").

The nucleotide sequence of vr2_1 as presently determined is reported in SEQ ID NO:99. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vr2_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vr2_1 should be approximately 1382 bp.

The nucleotide sequence disclosed herein for vr2_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No significant similarities were identified in the databases. The TopPredII computer program predicts a potential transmembrane domain within the vr2_1 protein sequence centered around amino acid 85 of SEQ ID NO:100. The nucleotide sequence of vr2_1 indicates that it may contain one ore more of the following repetitive elements: Alu, MER2, MER4B.

Clone "vc69_1"

A polynucleotide of the present invention has been identified as clone "vc69_1". vc69_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the

amino acid sequence of the encoded protein. vc69_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc69_1 protein").

The nucleotide sequence of vc69_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc69_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. Amino acids 7 to 19 of SEQ ID NO:102 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc69_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc69_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for vc69_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc69_1 demonstrated at least some similarity with sequences identified as AB023138 (Homo sapiens mRNA for KIAA0921 protein, partial cds), and AI421941 (tf45c01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE 2099136 3' similar to TR Q63376 Q63376 NEUREXIN II-BETA-A PRECURSOR; mRNA sequence). The predicted amino acid sequence disclosed herein for vc69_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vc69_1 protein demonstrated at least some similarity to sequences identified as AB02313 (KIAA0921 protein [Homo sapiens]), and various isoforms of *Rattus norvegicus* neurexin II protein. Based upon sequence similarity, vc69_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vc71_1"

A polynucleotide of the present invention has been identified as clone "vc71_1". vc71_1 was isolated from a human fetal brain cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vc71_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vc71_1 protein").

The nucleotide sequence of vc71_1 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vc71_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 2 to 14 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vc71_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vc71_1 should be approximately 760 bp.

The nucleotide sequence disclosed herein for vc71_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vc71_1 demonstrated at least some similarity with sequences identified as AI393859 (tg65f04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 2113663 3', mRNA sequence) and AL050018 (Homo sapiens mRNA; cDNA DKFZp564B116 (from clone DKFZp564B116)). Based upon sequence similarity, vc71_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo27_1"

A polynucleotide of the present invention has been identified as clone "vo27_1". vo27_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo27_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo27_1 protein").

The nucleotide sequence of vo27_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo27_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106. Amino acids 13 to 25 of SEQ ID NO:106 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 26. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the

predicted leader/signal sequence not be separated from the remainder of the vo27_1 protein.

Another potential reading frame, encoded by nucleotides 1665 to 1844 of SEQ ID NO:105, is reported as the amino acid sequence of SEQ ID NO:192. Amino acids 4 to 16 of SEQ ID NO:192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17; amino acids 28 to 40 of SEQ ID NO:192 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 41. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:192.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo27_1 should be approximately 2433 bp.

The nucleotide sequence disclosed herein for vo27_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo27_1 demonstrated at least some similarity with sequences identified as AC007621 (Homo sapiens clone RPCI11-757G14, WORKING DRAFT SEQUENCE, 142 unordered pieces), AI207832 (ao89g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE 1953092 3' similar to contains Alu repetitive element; mRNA sequence), and X80059 (Human PRO361 nucleotide sequence). Based upon sequence similarity, vo27_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo27_1 protein sequence centered around amino acid 400 of SEQ ID NO:106. The nucleotide sequence of vo27_1 indicates that it may contain an Alu repetitive element.

Clone "vo31_1"

A polynucleotide of the present invention has been identified as clone "vo31_1". vo31_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo31_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo31_1 protein").

The nucleotide sequence of vo31_1 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo31_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 7 to 19 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo31_1 protein.

Another potential reading frame, encoded by nucleotides 1937 to 3007 of SEQ ID NO:107, is reported as the amino acid sequence of SEQ ID NO:193.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo31_1 should be approximately 3222 bp.

The nucleotide sequence disclosed herein for vo31_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo31_1 demonstrated at least some similarity with sequences identified as AF022147 (Rattus norvegicus uterus-ovary specific putative transmembrane protein (uo) mRNA, complete cds), AI417638 (tg80e01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 2115096 3' similar to TR O35360 O35360 UTERUS-OVARY SPECIFIC PUTATIVE TRANSMEMBRANE PROTEIN; mRNA sequence), and X52248 (Protein PRO257 cDNA clone DNA35841-1173). The predicted amino acid sequence disclosed herein for vo31_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo31_1 protein demonstrated at least some similarity to sequences identified as AF02214 (uterus-ovary specific putative transmembrane protein [Rattus norvegicus]) and Y13377 (Amino acid sequence of protein PRO257). Based upon sequence similarity, vo31_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the protein sequence of SEQ ID NO:193, centered around amino acid 328 of SEQ ID NO:193. Hidden markov model analysis indicates the presence of Zona-pellucida-like domains at amino acids 26-115 and 146-273 of SEQ ID NO:193. The nucleotide sequence of vo31_1 indicates that it may contain a Mer5a repetitive element.

Clone "vo32_1"

A polynucleotide of the present invention has been identified as clone "vo32_1". vo32_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo32_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo32_1 protein").

The nucleotide sequence of vo32_1 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo32_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110. Amino acids 4 to 16 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 17. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo32_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo32_1 should be approximately 1868 bp.

The nucleotide sequence disclosed herein for vo32_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo32_1 demonstrated at least some similarity with sequences identified as AF028740 (Mus musculus olfactomedin mRNA, complete cds), AI078144 (oz30b06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE 1676819 3' similar to TR Q99784 Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; mRNA sequence), AI869993 (wl63e09.x1 NCI_CGAP Brn25 Homo sapiens cDNA clone IMAGE:2429608 3' similar to SW:NOMR_HUMAN Q99784 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN; mRNA sequence), and V34217 (Human secreted protein gene 64 clone HSLDJ95). The predicted amino acid sequence disclosed herein for vo32_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo32_1 protein demonstrated at least some similarity to sequences identified as U03416 (neuronal olfactomedin-related ER localized protein [Rattus norvegicus]) and W75120 (Human secreted protein encoded by gene 64 clone HSLDJ95). Based upon

sequence similarity, vo32_1 proteins and each similar protein or peptide may share at least some activity.

Clone "vo33_1"

A polynucleotide of the present invention has been identified as clone "vo33_1". vo33_1 was isolated from a human adult pancreas cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vo33_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vo33_1 protein").

The nucleotide sequence of vo33_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vo33_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 5 to 17 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vo33_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vo33_1 should be approximately 2879 bp.

The nucleotide sequence disclosed herein for vo33_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vo33_1 demonstrated at least some similarity with sequences identified as AI225613 (uj13e01.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1907928 5' similar to TR:Q14624 Q14624 INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN; mRNA sequence) and X80054 (Human PRO354 nucleotide sequence). The predicted amino acid sequence disclosed herein for vo33_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted vo33_1 protein demonstrated at least some similarity to sequences identified as D38535 (PK-120 precursor [Homo sapiens]), Y11545 (inter-alpha-inhibitor heavy-chain H2 [Sus scrofa]), and the H2 proteins of several species, including *Homo sapiens*. Based upon sequence similarity,

vo33_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the vo33_1 protein sequence centered around amino acid 386 of SEQ ID NO:112. The nucleotide sequence of vo33_1 indicates that it may contain an Alu repetitive element.

Clone "vq23_1"

A polynucleotide of the present invention has been identified as clone "vq23_1". vq23_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq23_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq23_1 protein").

The nucleotide sequence of vq23_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq23_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 18 to 30 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq23_1 protein.

Another potential reading frame, encoded by nucleotides 1012 to 1518 of SEQ ID NO:113, is reported as the amino acid sequence of SEQ ID NO:194. Amino acids 83 to 94 of SEQ ID NO:194 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 95. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of protein of SEQ ID NO:194.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq23_1 should be approximately 1793 bp.

The nucleotide sequence disclosed herein for vq23_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq23_1 demonstrated at least some similarity with sequences

identified as AA625521 (af72f02.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 1047579 5', mRNA sequence) and AC002364 (Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence). Based upon sequence similarity, vq23_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of vq23_1 indicates that it may contain an Alu repetitive element.

Clone "vq24_1"

A polynucleotide of the present invention has been identified as clone "vq24_1". vq24_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq24_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq24_1 protein").

The nucleotide sequence of vq24_1 as presently determined is reported in SEQ ID NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq24_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116. Amino acids 5 to 17 of SEQ ID NO:116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq24_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq24_1 should be approximately 2168 bp.

The nucleotide sequence disclosed herein for vq24_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq24_1 demonstrated at least some similarity with sequences identified as N29315 (yx43d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264491 5' similar to SP:SW:FCG1_HUMAN P12315 HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I 'B FORM' PRECURSOR; mRNA sequence). The predicted amino acid sequence disclosed herein for vq24_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX

search protocol. The predicted vq24_1 protein demonstrated at least some similarity to sequences identified as AF14317 (high affinity immunoglobulin gamma Fc receptor I [Mus musculus]) and R12428 (Hybrid Fc(gamma)RII/I receptor). Based upon sequence similarity, vq24_1 proteins and each similar protein or peptide may share at least some activity. Hidden markov model analysis detects immunoglobulin superfamily signatures in the vq24_1 protein sequence from amino acid 92 to amino acid 145, and from amino acid 185 to amino acid 242, of SEQ ID NO:116. The nucleotide sequence of vq24_1 indicates that it may contain one or more of the following repetitive elements: Mer, MLT1a.

Clone "vq26_1"

A polynucleotide of the present invention has been identified as clone "vq26_1". vq26_1 was isolated from a human adult lung cDNA library and was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. vq26_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "vq26_1 protein").

The nucleotide sequence of vq26_1 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the vq26_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118. Amino acids 9 to 21 of SEQ ID NO:118 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the vq26_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone vq26_1 should be approximately 1419 bp.

The nucleotide sequence disclosed herein for vq26_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. vq26_1 demonstrated at least some similarity with sequences identified as AA191552 (zp82g04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE 626742 3', mRNA sequence) and AA573741 (nk07a05.s1 NCI_CGAP_Co2

Homo sapiens cDNA clone IMAGE:1012784 3', mRNA sequence). Based upon sequence similarity, vq26_1 proteins and each similar protein or peptide may share at least some activity.

Deposit of Clones

Clones vc62_1, vp10_1, vp11_1, vp13_1, vp16_1, vp21_1, vp22_1, vq2_1, vq3_1, vq5_1, vq6_1, and vr1_1 were deposited on February 17, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 207114, from which each clone comprising a particular polynucleotide is obtainable.

Clone vc63_1 was deposited on February 17, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number ATCC 207115, from which the vc63_1 clone comprising a particular polynucleotide is obtainable.

Clones vb25_1, vb27_1, vb28_1, vb29_1, vb30_1, vc67_1, vf4_1, vg3_1, vo2_1, vo3_1, vo5_1, vo6_1, and vo9_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-362, from which each clone comprising a particular polynucleotide is obtainable.

Clones vo11_1, vo12_1, vo13_1, vo14_1, vo15_1, vo16_1, vo18_1, vo19_1, vo22_1, vo23_1, vo24_1, vo25_1, and vo26_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-366, from which each clone comprising a particular polynucleotide is obtainable.

Clones vp23_1, vq7_1, vq8_1, vq9_1, vq10_1, vq13_1, vq16_1, vq19_1, vq20_1, vq21_1, and vr2_1 were deposited on July 15, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.)

as an original deposit under the Budapest Treaty and were given the accession number PTA-368, from which each clone comprising a particular polynucleotide is obtainable.

Clones vc69_1, vc71_1, vo27_1, vo31_1, vo32_1, vo33_1, vq23_1, vq24_1, and vq26_1 were deposited on December 21, 1999 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number PTA-1075, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in these composite deposits. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* **19**: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* **9**: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

Clone	Probe Sequence
vc62_1	SEQ ID NO:119
vp10_1	SEQ ID NO:120
vp11_1	SEQ ID NO:121
vp13_1	SEQ ID NO:122
vp16_1	SEQ ID NO:123
vp21_1	SEQ ID NO:124
vp22_1	SEQ ID NO:125
vq2_1	SEQ ID NO:126
vq3_1	SEQ ID NO:127
vq5_1	SEQ ID NO:128
vq6_1	SEQ ID NO:129
vr1_1	SEQ ID NO:130
vc63_1	SEQ ID NO:131
vb25_1	SEQ ID NO:132
vb27_1	SEQ ID NO:133
vb28_1	SEQ ID NO:134
vb29_1	SEQ ID NO:135
vb30_1	SEQ ID NO:136
vc67_1	SEQ ID NO:137
vf4_1	SEQ ID NO:138
vg3_1	SEQ ID NO:139
vo2_1	SEQ ID NO:140
vo3_1	SEQ ID NO:141
vo5_1	SEQ ID NO:142
vo6_1	SEQ ID NO:143
vo9_1	SEQ ID NO:144
vo11_1	SEQ ID NO:145
vo12_1	SEQ ID NO:146
vo13_1	SEQ ID NO:147
vo14_1	SEQ ID NO:148
vo15_1	SEQ ID NO:149

vo16_1	SEQ ID NO:150
vo18_1	SEQ ID NO:151
vo19_1	SEQ ID NO:152
vo22_1	SEQ ID NO:153
vo23_1	SEQ ID NO:154
vo24_1	SEQ ID NO:155
vo25_1	SEQ ID NO:156
vo26_1	SEQ ID NO:157
vp23_1	SEQ ID NO:158
vq7_1	SEQ ID NO:159
vq8_1	SEQ ID NO:160
vq9_1	SEQ ID NO:161
vq10_1	SEQ ID NO:162
vq13_1	SEQ ID NO:163
vq16_1	SEQ ID NO:164
vq19_1	SEQ ID NO:165
vq20_1	SEQ ID NO:166
vq21_1	SEQ ID NO:167
vr2_1	SEQ ID NO:168

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoaramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramadite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

(a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

(b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ-^{32}P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for

labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 μg/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 μg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. “Corresponding genes” are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An “isolated gene” is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address http://www.ncbi.nlm.nih.gov/UniGene/, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* **15(7)**: 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* **62(1)**: 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA intereference" or "RNAi"; Fire *et al.*, 1998, *Nature* **391** (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* **95** (26): 15502-15507; and Sharp, 1999, *Genes Dev.* **13** (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European

Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* **14(9)**: 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90(16)**: 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91(2)**: 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* **336**: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmsmbrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid

sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed., Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from ftp://blast.wustl.edu/blast/executables. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any

combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* **22**: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* **3**:103-112; Johansson *et al.*, 1995, *Genomics* **25**: 682-690; Lyons *et al.*, 1997, *Nature Genetics* **15**: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* **13(10)**: 393-399; Carver and Stubbs, 1997, *Genome Research* **7**:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp)[‡]	Hybridization Temperature and Buffer[†]	Wash Temperature and Buffer[†]
A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
B	DNA:DNA	<50	T_B*; 1xSSC	T_B*; 1xSSC
C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
D	DNA:RNA	<50	T_D*; 1xSSC	T_D*; 1xSSC
E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
F	RNA:RNA	<50	T_F*; 1xSSC	T_F*; 1xSSC
G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
H	DNA:DNA	<50	T_H*; 4xSSC	T_H*; 4xSSC
I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
J	DNA:RNA	<50	T_J*; 4xSSC	T_J*; 4xSSC
K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
L	RNA:RNA	<50	T_L*; 2xSSC	T_L*; 2xSSC
M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
N	DNA:DNA	<50	T_N*; 6xSSC	T_N*; 6xSSC
O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
P	DNA:RNA	<50	T_P*; 6xSSC	T_P*; 6xSSC
Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
R	RNA:RNA	<50	T_R*; 4xSSC	T_R*; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6($\log_{10}$[Na^+]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide endcoing the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable

bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium,* or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope.

One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell*

75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* **94**: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology.* J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In *Current Protocols in Immunology.* J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology.* J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al.,

Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology.* J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology.* J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology.* J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,

in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble,

monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science *257*:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, *89*:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the

disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an

expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol.

137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz

et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc.., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone

fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

<u>Hemostatic and Thrombolytic Activity</u>

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation

and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for h mophilic adhesion; modification of this recognition site can change the specificity of a cadherin

so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and poly-nucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the

circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the

term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, Monoclonal antibodies: principles and practice, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in Current Protocols in Immunology, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, supra; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in Current Protocols in Immunology, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* **14**: 845-851; Mendez *et al.*, 1997, *Nature Genetics* **15**: 146-156 (erratum *Nature Genetics* **16**: 410)); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics.

Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be

formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:1;

(b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 27 to nucleotide 260;

(c) the nucleotide sequence of SEQ ID NO:1 from nucleotide 72 to nucleotide 260;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc62_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:1.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.

4. The host cell of claim 3, wherein said cell is a mammalian cell.

5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

(a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and

(b) purifying said protein from the culture.

6. A protein produced according to the process of claim 5.

7. An isolated polynucleotide encoding the protein of claim 6.

8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114.

9. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc62_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:3;

(b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 6 to nucleotide 1325;

(c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 99 to nucleotide 1325;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp10_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp10_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:5;

(b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 149 to nucleotide 322;

(c) the nucleotide sequence of SEQ ID NO:5 from nucleotide 200 to nucleotide 322;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp11_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp11_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:7;

(b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 288 to nucleotide 629;

(c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 363 to nucleotide 629;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp13_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp13_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:9;

(b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 11 to nucleotide 298;

(c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 149 to nucleotide 298;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp16_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp16_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:11;

(b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 257 to nucleotide 607;

(c) the nucleotide sequence of SEQ ID NO:11 from nucleotide 479 to nucleotide 607;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp21_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp21_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:13;

(b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 163 to nucleotide 477;

(c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 238 to nucleotide 477;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp22_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:14;

(b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp22_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:15;

(b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 58 to nucleotide 624;

(c) the nucleotide sequence of SEQ ID NO:15 from nucleotide 106 to nucleotide 624;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq2_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq2_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:17;

(b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 773 to nucleotide 1090;

(c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 842 to nucleotide 1090;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq3_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq3_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:19;

(b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 96 to nucleotide 275;

(c) the nucleotide sequence of SEQ ID NO:19 from nucleotide 159 to nucleotide 275;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq5_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq5_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:21;

(b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 176 to nucleotide 340;

(c) the nucleotide sequence of SEQ ID NO:21 from nucleotide 230 to nucleotide 340;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq6_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq6_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:23;

(b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 29 to nucleotide 1111;

(c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 167 to nucleotide 1111;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(f) the nucleotide sequence of a mature protein coding sequence of clone vr1_1 deposited with the ATCC under accession number 207114;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

(b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone vr1_1 deposited with the ATCC under accession number 207114;

the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:25;

(b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 13 to nucleotide 513;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vc63_1 deposited with the ATCC under accession number 207115;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:26;

(b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc63_1 deposited with the ATCC under accession number 207115;

the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:27;

(b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 79 to nucleotide 345;

(c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 130 to nucleotide 345;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb25_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:29;

(b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 72 to nucleotide 236;

(c) the nucleotide sequence of SEQ ID NO:29 from nucleotide 150 to nucleotide 236;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb27_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:31;

(b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 884;

(c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 183 to nucleotide 884;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:32;

(b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb28_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:33;

(b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 42 to nucleotide 206;

(c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 111 to nucleotide 206;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:34;

(b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and

(c) the amino acid sequence encoded by the cDNA insert of clone vb29_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 17 to nucleotide 253;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 98 to nucleotide 253;

(c) the amino acid sequence encoded by the cDNA insert of clone vb30_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:37;

(b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 68 to nucleotide 424;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:38;

(b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc67_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:39;

(b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 103 to nucleotide 261;

(c) the nucleotide sequence of SEQ ID NO:39 from nucleotide 154 to nucleotide 261;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone vf4_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:41;

(b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1575 to nucleotide 3038;

(c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1650 to nucleotide 3038;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(c) the amino acid sequence encoded by the cDNA insert of clone vg3_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:43;

(b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 2112 to nucleotide 2363;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:44;

(b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo2_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:45;

(b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 36 to nucleotide 707;

(c) the nucleotide sequence of SEQ ID NO:45 from nucleotide 393 to nucleotide 707;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo3_1 deposited with the ATCC under accession number PTA-362;

(c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 134 to nucleotide 295;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:48;

(b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo5_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:49;

(b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 45 to nucleotide 383;

(c) the nucleotide sequence of SEQ ID NO:49 from nucleotide 312 to nucleotide 383;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:50;

(b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo6_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:51;

(b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 186 to nucleotide 1739;

(c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 288 to nucleotide 1739;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

(b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo9_1 deposited with the ATCC under accession number PTA-362;

the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:53;

(b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 440 to nucleotide 835;

(c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 632 to nucleotide 835;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo11_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:55;

(b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 72 to nucleotide 329;

(c) the nucleotide sequence of SEQ ID NO:55 from nucleotide 120 to nucleotide 329;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo12_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:57;

(b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 227 to nucleotide 439;

(c) the nucleotide sequence of SEQ ID NO:57 from nucleotide 287 to nucleotide 439;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo13_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:59;

(b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 96 to nucleotide 341;

(c) the nucleotide sequence of SEQ ID NO:59 from nucleotide 174 to nucleotide 341;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo14_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:61;

(b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 90 to nucleotide 599;

(c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 165 to nucleotide 599;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo15_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:63;

(b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 209 to nucleotide 451;

(c) the nucleotide sequence of SEQ ID NO:63 from nucleotide 398 to nucleotide 451;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:64;

(b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo16_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:65;

(b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 31 to nucleotide 231;

(c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 97 to nucleotide 231;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

75. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:66;

(b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo18_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:67;

(b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 23 to nucleotide 736;

(c) the nucleotide sequence of SEQ ID NO:67 from nucleotide 83 to nucleotide 736;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:68;

(b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo19_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:69;

(b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 104 to nucleotide 1399;

(c) the nucleotide sequence of SEQ ID NO:69 from nucleotide 158 to nucleotide 1399;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:69.

79. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo22_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:71;

(b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 174 to nucleotide 1595;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:71.

81. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo23_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:73;

(b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 129 to nucleotide 311;

(c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 195 to nucleotide 311;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:74;

(b) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo24_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:75;

(b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 73 to nucleotide 798;

(c) the nucleotide sequence of SEQ ID NO:75 from nucleotide 142 to nucleotide 798;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:76;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:75.

85. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:76;

(b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo25_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:27;

(b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 26 to nucleotide 307;

(c) the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 307;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:78;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:27.

87. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:78;

(b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo26_1 deposited with the ATCC under accession number PTA-366;

the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:79;

(b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 43 to nucleotide 228;

(c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 94 to nucleotide 228;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone vp23_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:81;

(b) the nucleotide sequence of SEQ ID NO:81 from nucleotide 245 to nucleotide 427;

(c) the nucleotide sequence of SEQ ID NO:81 from nucleotide 308 to nucleotide 427;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:81.

91. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:82;

(b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq7_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:83;

(b) the nucleotide sequence of SEQ ID NO:83 from nucleotide 119 to nucleotide 475;

(c) the nucleotide sequence of SEQ ID NO:83 from nucleotide 185 to nucleotide 475;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:83.

93. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:84;

(b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq8_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:85;

(b) the nucleotide sequence of SEQ ID NO:85 from nucleotide 90 to nucleotide 323;

(c) the nucleotide sequence of SEQ ID NO:85 from nucleotide 141 to nucleotide 323;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:85.

95. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:86;

(b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq9_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:87;

(b) the nucleotide sequence of SEQ ID NO:87 from nucleotide 18 to nucleotide 452;

(c) the nucleotide sequence of SEQ ID NO:87 from nucleotide 72 to nucleotide 452;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:88;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:87.

97. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;

(b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq10_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:89;

(b) the nucleotide sequence of SEQ ID NO:89 from nucleotide 196 to nucleotide 378;

(c) the nucleotide sequence of SEQ ID NO:89 from nucleotide 262 to nucleotide 378;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:89.

99. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:90;

(b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq13_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:91;

(b) the nucleotide sequence of SEQ ID NO:91 from nucleotide 35 to nucleotide 718;

(c) the nucleotide sequence of SEQ ID NO:91 from nucleotide 173 to nucleotide 718;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:92;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:91.

101. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:92;

(b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq16_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

102. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:93;

(b) the nucleotide sequence of SEQ ID NO:93 from nucleotide 1 to nucleotide 762;

(c) the nucleotide sequence of SEQ ID NO:93 from nucleotide 70 to nucleotide 762;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:93.

103. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:94;

(b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq19_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:95;

(b) the nucleotide sequence of SEQ ID NO:95 from nucleotide 106 to nucleotide 792;

(c) the nucleotide sequence of SEQ ID NO:95 from nucleotide 172 to nucleotide 792;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:95.

105. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

(b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq20_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:97;

(b) the nucleotide sequence of SEQ ID NO:97 from nucleotide 40 to nucleotide 315;

(c) the nucleotide sequence of SEQ ID NO:97 from nucleotide 124 to nucleotide 315;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID-NO:98;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:97.

107. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:98;

(b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq21_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:99;

(b) the nucleotide sequence of SEQ ID NO:99 from nucleotide 70 to nucleotide 699;

(c) the nucleotide sequence of the full-length protein coding sequence of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:100;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:99.

109. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:100;

(b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and

(c) the amino acid sequence encoded by the cDNA insert of clone vr2_1 deposited with the ATCC under accession number PTA-368;

the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:101;

(b) the nucleotide sequence of SEQ ID NO:101 from nucleotide 170 to nucleotide 394;

(c) the nucleotide sequence of SEQ ID NO:101 from nucleotide 227 to nucleotide 394;

(d) the nucleotide sequence of the full-length protein coding sequence of clone PTA-1075 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:102;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:101.

111. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:102;

(b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc69_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:103;

(b) the nucleotide sequence of SEQ ID NO:103 from nucleotide 43 to nucleotide 198;

(c) the nucleotide sequence of SEQ ID NO:103 from nucleotide 85 to nucleotide 198;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:103.

113. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:104;

(b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and

(c) the amino acid sequence encoded by the cDNA insert of clone vc71_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:105;

(b) the nucleotide sequence of SEQ ID NO:105 from nucleotide 260 to nucleotide 1552;

(c) the nucleotide sequence of SEQ ID NO:105 from nucleotide 335 to nucleotide 1552;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:105.

115. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo27_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:107;

(b) the nucleotide sequence of SEQ ID NO:107 from nucleotide 15 to nucleotide 320;

(c) the nucleotide sequence of SEQ ID NO:107 from nucleotide 72 to nucleotide 320;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:108;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:107.

117. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:108;

(b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo31_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:109;

(b) the nucleotide sequence of SEQ ID NO:109 from nucleotide 38 to nucleotide 1255;

(c) the nucleotide sequence of SEQ ID NO:109 from nucleotide 86 to nucleotide 1255;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:110;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:109.

119. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:110;

(b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo32_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:111;

(b) the nucleotide sequence of SEQ ID NO:111 from nucleotide 80 to nucleotide 1276;

(c) the nucleotide sequence of SEQ ID NO:111 from nucleotide 131 to nucleotide 1276;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:111.

121. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:112;

(b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and

(c) the amino acid sequence encoded by the cDNA insert of clone vo33_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:113;

(b) the nucleotide sequence of SEQ ID NO:113 from nucleotide 202 to nucleotide 429;

(c) the nucleotide sequence of SEQ ID NO:113 from nucleotide 292 to nucleotide 429;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:114;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:113.

123. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:114;

(b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq23_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

124. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:115;

(b) the nucleotide sequence of SEQ ID NO:115 from nucleotide 37 to nucleotide 1113;

(c) the nucleotide sequence of SEQ ID NO:115 from nucleotide 88 to nucleotide 1113;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:115.

125. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

(b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq24_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:117;

(b) the nucleotide sequence of SEQ ID NO:117 from nucleotide 40 to nucleotide 207;

(c) the nucleotide sequence of SEQ ID NO:117 from nucleotide 103 to nucleotide 207;

(d) the nucleotide sequence of the full-length protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(f) the nucleotide sequence of a mature protein coding sequence of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:118;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:117.

127. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone vq26_1 deposited with the ATCC under accession number PTA-1075;

the protein being substantially free from other mammalian proteins.

Fig. 1A

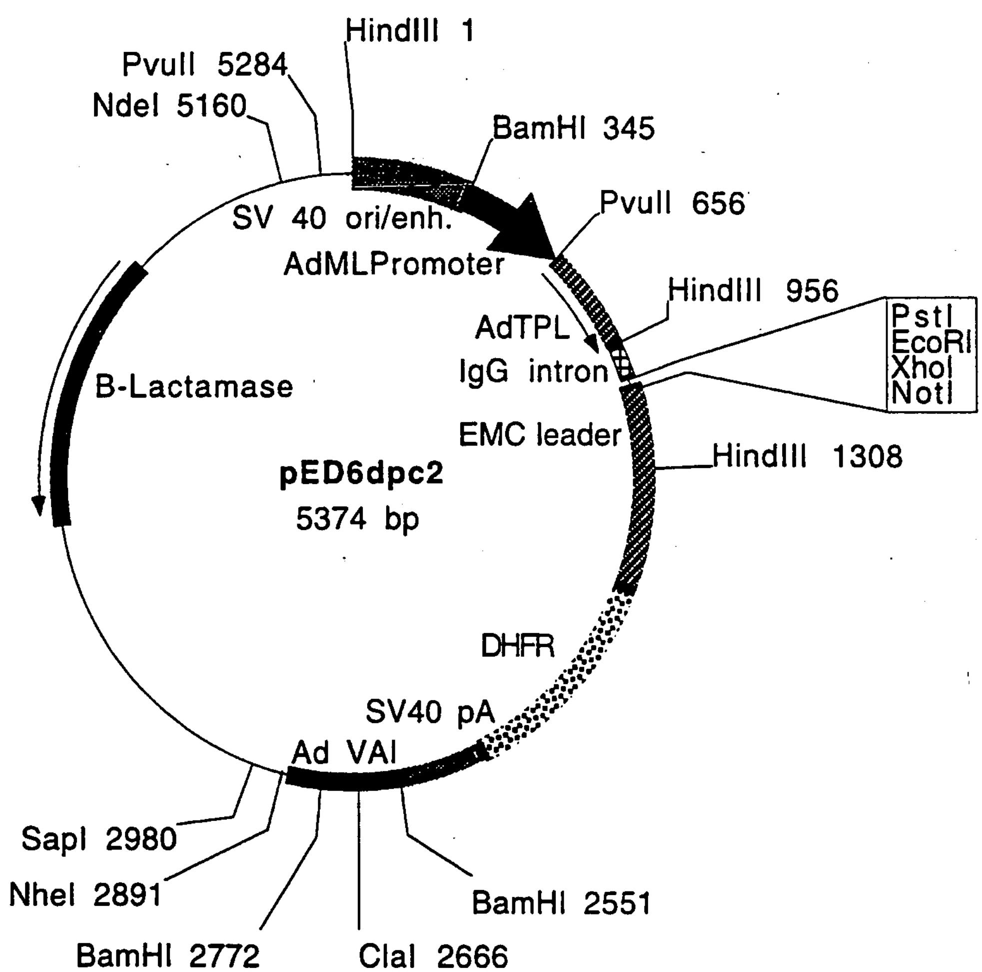
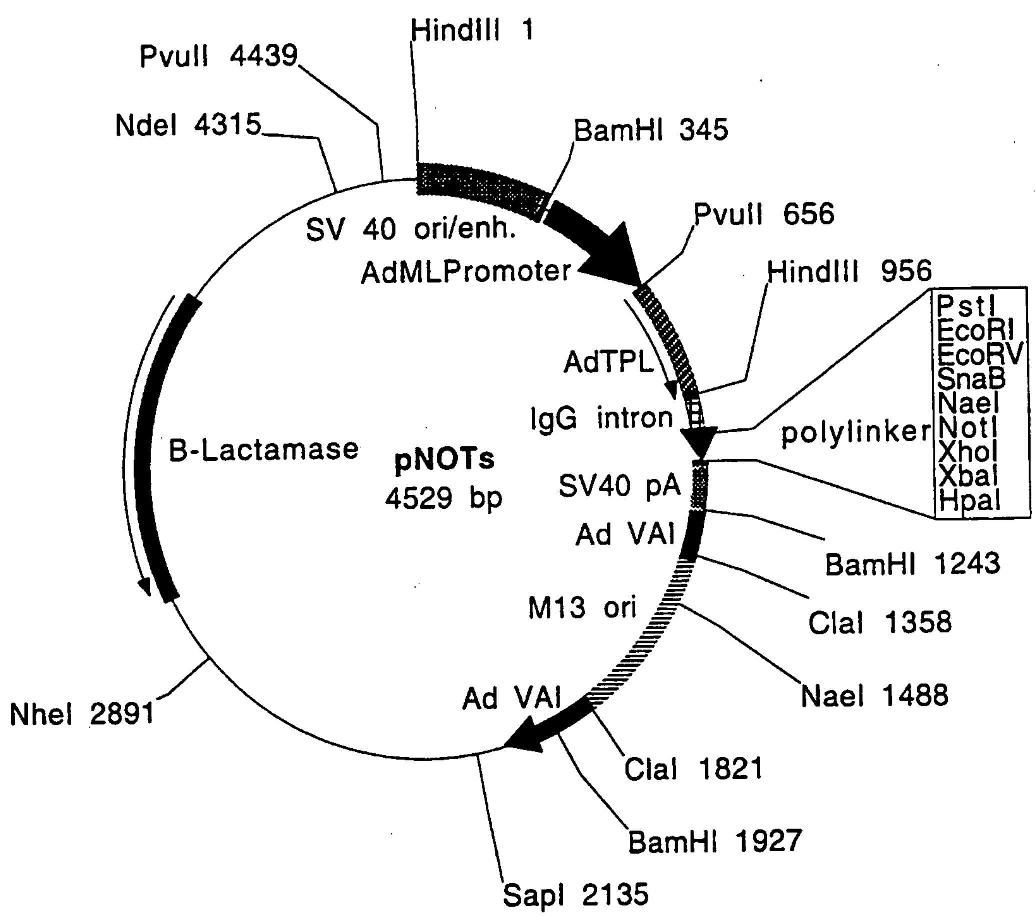

HindIII 1
PvuII 5284
NdeI 5160
BamHI 345
PvuII 656
SV 40 ori/enh.
AdMLPromoter
HindIII 956
AdTPL
IgG intron
PstI
EcoRI
XhoI
NotI
B-Lactamase
EMC leader
HindIII 1308
pED6dpc2
5374 bp
DHFR
SV40 pA
Ad VAI
SapI 2980
NheI 2891
BamHI 2772
ClaI 2666
BamHI 2551

Fig. 1B


HindIII 1
PvuII 4439
NdeI 4315
BamHI 345
SV 40 ori/enh.
AdMLPromoter
PvuII 656
HindIII 956
AdTPL
IgG intron
polylinker
PstI
EcoRI
EcoRV
SnaB
NaeI
NotI
XhoI
XbaI
HpaI
B-Lactamase
pNOTs
4529 bp
SV40 pA
Ad VAI
BamHI 1243
M13 ori
ClaI 1358
NaeI 1488
Ad VAI
NheI 2891
ClaI 1821
BamHI 1927
SapI 2135

SEQUENCE LISTING

<110> Valenzuela, Dario
Yuan, Olive
Hoffman, Heidi
Hall, Jeff
Rapiejko, Peter

<120> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

<130> GI 6919X

<140>
<141>

<160> 194

<170> PatentIn Ver. 2.0

<210> 1
<211> 4177
<212> DNA
<213> Homo sapiens

<400> 1
gttaaagggt aaccccatgc cttggaatgg tattaaccct gtggtgcaat ttgtgctcca 60
gagcttcctc atgggtgaga cagaagcacg tgtcctgttg tgtccacaac tacactcagc 120
ctttttgct cattcaatcc tcattttggg ctatgtcttc agaaactaaa ccgaaggcac 180
tatccaaaga ttacttgtgt atttcttata gaagccccca ctccaccccc acacacagac 240
attcctcaaa taggttccta tgacctacca gttgaagccc aggcttctta tctggacatt 300
aagtctttgc atggtcagtc gggtctctgt ctttcaagat ttatttttca ctatcataca 360
ccatattaac ctactcaggg ctgcctactt tacattctct cccagccctg cacattcctt 420
ggaaaggcct cccctgcctc gcctgaatga tgaacactct attccttatt caagactcta 480
acatcacttg ccctgtgaag gctcctcaga ttcctctagg ctcagtaggt gccactcctc 540
agtcccctac agcatatggt gtcaatgaca acagtgatat gcttgtctga ttcctccact 600
taactatgaa ttttttgttg ttgttaataa aaacgtttat tttgcatttt atacagaacc 660
gcctgaagtc tgcatcatga cttgatggtt acccaggggt ttatgtgtgt ccaactgaac 720
accgtggttc tgggattgag gatccgcaca aacacaggca ggagtttgga gggaagaagg 780
gggcacagca ggagtgtatc tcaagcccac ctcaaaggca gcagagcatt ccaagttgct 840
gaaaacctgt gcaaatgggg cctctaaaac aaacattgta ctgtgagctc tcggggaagg 900
ggcaggaaaa ggatgttgat aattaagggg gcattttctt gaggcggcag atgaggaggg 960
aggcttacta tttttaatcc cctcagcccc aggacatgat aatcagagga gatcatgtcc 1020
aatcttgaat caattccctg ttcaaaaaga ggtgctaata ccccagggac cagactctga 1080
aaataccatg aaaatactct gaaaataccg tgctggtcat tcctgagtcc ctgttctatg 1140
ccctacaaca tattagaagg gcaagggaag gtcagagggt agtggcttgt gttctgtgga 1200
agtaaaacac cttagttcat attaagcact gataaaaccc aatgactggg accacagatc 1260
tgttgagagg tcactagtag ggaccaagag tgggaggtct ggaacatcct cagcttgaga 1320
tgcagtaggt gtggaaagtc tgggaggagg taaatattaa agtaatggga aacagaacac 1380
tcccaagcct taattttaat tggatagttt aaaaaattga aatagaatct aacattgggt 1440
gccagtcacc acaaatgcca tgcctttatg gtcacttggt atcataaaaa atttgccaaa 1500
gcatgcctgt ctggctaatc aaaaggtctt gctaggaggt gttcgtgtgc atgacagagt 1560
gccaaggggc ttggtaccac tgactatcca acgtgattcc tatggaaaca gaagcggcag 1620
agtcttggtt agctggcttg ttgaggtttg gcagagaaga agcgaaagct ccaaagtgac 1680
tgcagattct ctgcaactgg ctttgaccca gagaaagagg agccacattc tcactctaaa 1740
gatagagagg gaccaaacct aacccacagc acatgcatta gttctggtca tcctacagtt 1800
gatgggcaac taacactggg caggggaagg gagctggtta gggaagaagg gctcattttt 1860
catttttaa agtcttaatt aatattttaa cctcaaacag attatcagtg cctcagatac 1920
aatttaatct taagtcttta aaaggccccc tgaaacaaaa atatacattt ttttaaggca 1980
tcctcacttt ctgatagtca gtttccccca gtctccagtt ttaccctgac ttagagtcca 2040
caaacttcat cagaccacct gtgctcatgg acgtgggtct ttctagaggg aagcctcggg 2100

ctcggctcca gatgagctgt gccagtacac ccaatgcctg tgatgcccca aacaggaccg 2160
cgtagcaatg tatctctgtc atgctatagt acccaccatg tgcgtctaca ttgggcccag 2220
gattctcggc cttaccctac tgtcagagga tattgggcac aatcttgtat agctgagcaa 2280
ccaacttaaa catgggatca ttatgcaatg tttcagagca aactctcgct gacaggtaca 2340
ttgtggctca gtcttcttta gtactgcatg gccatagcct ggaacaaccc atctcgagtt 2400
cagtgtagtc ttgtaacttc tcatctgaca catctttgcc aacttccttc tgtagttgtg 2460
ttagccagac aagcacttcc tgatttgcca gtccatgtag aggaactgcc agcccattca 2520
tggctgctgc aaagggcagg gaagggtctg aaagggtact gcctgccaaa tgcctggcat 2580
gagcacttat attgctgtgc tcatggtcac tgtggatggt gagctacagg tgcatgagct 2640
cagtgaactg agcatcagta tagcctaaca tgttggtgaa actgtgggac cagtccagct 2700
tagagtcagt gaccccaata ccactgccct ctccacagag attttggtag accttttctg 2760
caatacaagg tagctttgtg attagacaca catggtcttc ataaatcaac tcccagtact 2820
tggtttgact ggcaccctct ggatatgctc gggcaaagtt gtttagggct gccatggctg 2880
cagtgggctc agacatgggt gtggattggt gggaaagttg tccagcatgg tgaccacatg 2940
ggaaggtaga gctgcctgcc ctctttgccc actctcttaa aagccaagat acctgttcct 3000
ctcttgggat ctgtccagtt accagcagcc aaaataagcc cctgggtagg ggttttcccc 3060
acccttagtc ttgggtagca gttttggtat tcagggatac tgaagcctcg gaaacagata 3120
acctcatcag gatcaagaac tgatgtttat ataccaatcc cttaatgcct ctcatgccgc 3180
catacattat gtctgcagtg atttggccca ccaccttctt gccatgttgc tgcctgaagg 3240
tcttaattct ggcctgctcc ttaactatca ggtcagccaa tatgtctttc aaattcttgg 3300
aggaagcact ggcatgccag gcagcaagaa caagacaaga tgcactgttg cttcccaaga 3360
gcctggcagc cacttgggta aaaccatggt gagtgaactc tgcgatctgg tggagaggga 3420
agaaggggag agagctgtgg cagaaacagg aaccaccact gcggcaccag aggccgcaat 3480
gggtggacaa ggttgaaagg aggcagctga ggaaacacat agatgaaccc gcagcaggtg 3540
cccagccagg ggttctcagc aaggccctgt gcactgccaa ctatgaactt attaagactg 3600
actttccaat agttcttagc agtgtgtgga gtagaagaca gaacaacgta taccttcaga 3660
atgcacagag ccaatgcatt tttggattac aaataaatca atttaagacc tattgcttct 3720
gacaatgatt tgcaaattga gaaaattctg gaaaaataga catccaacaa attaacagtg 3780
attatacсta atgacagggt tacaggtggg gatttgttta tttgtatgtt cttatttgtt 3840
tcttgtttct tatgtcagca aattttaaat agaatatgca aaatgatgac ctcaataata 3900
aaaaatattg tgtttattca caagagttaa ataatgttta tagaaaggaa aagatgcgaa 3960
tgtttttgga cagattagga tttaaacaaa aatgttaaac acagaataca aaatatgttt 4020
tttctcctgt tgtctagctt ttgtacagtg aacacatgtt gcttttatag taagaaatat 4080
acattttaag tttcaaaatt actcagattt tgtaaacaat ctaaaagaaa ataaatgtgt 4140
ttggaaaatc caaaaaaaaa aaaaaaaaaa aaaaaaa 4177

<210> 2
<211> 78
<212> PRT
<213> Homo sapiens

<400> 2
Met Val Leu Thr Leu Trp Cys Asn Leu Cys Ser Arg Ala Ser Ser Trp
1 5 10 15

Val Arg Gln Lys His Val Ser Cys Cys Val His Asn Tyr Thr Gln Pro
20 25 30

Phe Leu Leu Ile Gln Ser Ser Phe Trp Ala Met Ser Ser Glu Thr Lys
35 40 45

Pro Lys Ala Leu Ser Lys Asp Tyr Leu Cys Ile Ser Tyr Arg Ser Pro
50 55 60

His Ser Thr Pro Thr His Arg His Ser Ser Asn Arg Phe Leu
65 70 75

<210> 3
<211> 1326

<212> DNA
<213> Homo sapiens

<400> 3
gggagatggc agtgagcgag aggaggggc tcggccgcgg gagccccgcg gagtgggggc 60
agcggctact tctggtgctg ctgttgggtg gctgctccgg gcgcatccac cggctggcgc 120
tgacgggga gaagcgagcg gacatccagc tgaacagctt cggtttctac accaatggct 180
ctctggaggt ggagttgagc gtcctgcggc tgggcctccg ggaggcagaa gagaagtccc 240
tgctggtggg gttcagtctc agccgggttc ggtctggcag agttcgctcc tattcaaccc 300
gggatttcca ggactgccct ctccagaaaa acagtagcag tttcctggtc ctgttcctca 360
tcaacaccaa ggatctgcag gtccaggtgc ggaagtatgg agagcagaag acgttgttta 420
tctttcccgg gctcctcccg gaagcaccct ccaaaccagg gctcccgaag ccacaggcca 480
cagtcccccg caaggtggat ggcggaggga cctctgcagc cagcaagccc aagtcaacac 540
ccgcagtgat tcagggtcct agtgggaagg acaaggacct ggtgttgggc ctgagccacc 600
tcaacaactc ctacaacttc agtttccacg tggtgatcgg ctctcaggcg gaagaaggcc 660
agtacagcct gaacttccac aactgcaaca attcagtgcc aggaaaggag catccattcg 720
acatcacggt gatgatccgg gagaagaacc ccgatggctt cctgtcggca gcggagatgc 780
ccctttttcaa gctctacatg gtcatgtccg cctgcttcct ggccgctggc agtggctgta 840
ccagctcttg gtggagggct ccaccctgcc ttcttcgtgc tcacgggcta caagttccag 900
cccacaggaa acaacccgta cctgcagctg ccccaggagg acgaggagga tgttcagatg 960
gagcaagtaa tgacggactc tgggttccgg gaaggcctct ccaaagtcaa caaaacagcc 1020
agcgggcggg aactgttatg atcacctcca catctcagac caaagggtcg tcctccccca 1080
gcatttctca ctcctgccct tcttccacag cgtatgtggg gaggtggagg gggtccatgt 1140
ggaccaggcg cccagctccc cgggaccccg gttcccggac aagcccattt ggaagaagag 1200
tcccttcctc cccccaaata ttgggcagcc ctgtccttac cccgggacca cccctccctt 1260
ccagctatgt gtacaataat gaccaatctg tttggctaaa aaaaaaaaa aaaaaaaaaa 1320
aaaaaa 1326

<210> 4
<211> 440
<212> PRT
<213> Homo sapiens

<400> 4
Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu
1 5 10 15

Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly
20 25 30

Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln
35 40 45

Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu
50 55 60

Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu
65 70 75 80

Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr
85 90 95

Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser
100 105 110

Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val
115 120 125

Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu
130 135 140

```
Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val
145                 150                 155                 160

Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys
                165                 170                 175

Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu
            180                 185                 190

Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His
        195                 200                 205

Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe
    210                 215                 220

His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile
225                 230                 235                 240

Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala
                245                 250                 255

Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu
            260                 265                 270

Ala Ala Gly Ser Gly Cys Thr Ser Ser Trp Trp Arg Ala Pro Pro Cys
        275                 280                 285

Leu Leu Arg Ala His Gly Leu Gln Val Pro Ala His Arg Lys Gln Pro
    290                 295                 300

Val Pro Ala Ala Ala Pro Gly Gly Arg Gly Gly Cys Ser Asp Gly Ala
305                 310                 315                 320

Ser Asn Asp Gly Leu Trp Val Pro Gly Arg Pro Leu Gln Ser Gln Gln
                325                 330                 335

Asn Ser Gln Arg Ala Gly Thr Val Met Ile Thr Ser Thr Ser Gln Thr
            340                 345                 350

Lys Gly Ser Ser Ser Pro Ser Ile Ser His Ser Cys Pro Ser Ser Thr
        355                 360                 365

Ala Tyr Val Gly Arg Trp Arg Gly Ser Met Trp Thr Arg Arg Pro Ala
    370                 375                 380

Pro Arg Asp Pro Gly Ser Arg Thr Ser Pro Phe Gly Arg Arg Val Pro
385                 390                 395                 400

Ser Ser Pro Gln Ile Leu Gly Ser Pro Val Leu Thr Pro Gly Pro Pro
                405                 410                 415

Leu Pro Ser Ser Tyr Val Tyr Asn Asn Asp Gln Ser Val Trp Leu Lys
            420                 425                 430

Lys Lys Lys Lys Lys Lys Lys Lys
        435                 440
```

<210> 5

<211> 1280
<212> DNA
<213> Homo sapiens

<400> 5
aaaggggcta attggagatc tgtgagttta atgagcttga gtctcttctt cacaccagag 60
actgatgttt tctgggtagc aggggagcca gtaccttctt tttctcagta agtatctttc 120
tagtcacctg aggattttgg gagacagaat ggagaatgaa ttgattgcct tgggtgcctc 180
attcagggat gtgacagcag ctagtacaca ctgcatttgt gataaggctg atacgaggga 240
caacagaggg tacgttttct tgaagatgta tcttgtaaaa gaaaaaaatc ctttatttat 300
atatgatgga aagcttggaa catagcacca ctccctttag aacttgtgtg tgaaaatgag 360
caattagtgg acatttagat ggtgcttaaa tgagcaagtt ttcctgatta tagcctaaca 420
gagaaatcag aaagtgacca atataacatg ttttgttgac aaactaaaag catacacatt 480
agcagcatat ctctgtagaa ccttcacttc atgcttgact atcatgtatt ttgagtttgc 540
aaagaaatag ctggacagtc cagaagctat ctggctcaga catccattta tctcaggctg 600
tgtagagtgc tacacaggaa gaccacagca gcagcatcac ctggaacttc atagaaatgc 660
agattcttgg gctccattgc agacctaaga aatcagaatc tgcattttaa taagaccccc 720
ccaaagcaat ttgagtgcac attaaagctt aagaaacact ggttggtcta ggccgggcgt 780
ggtggcttat gcctgtgatc ccagcacttt gggaggccaa ggcgggcaga tcacgaggtc 840
aggagattga gaacatcctg gctagcatgg tgaaaccccg tctctgctaa aaatacaaaa 900
aattagccag gcgtggtggc gggcgcctgt agtcccagct acttgggagg ctgaggcagc 960
agaatggcat gaacccggga ggcagagctt tcggtgagcc cagatggcgc cactgcactc 1020
cagcctgggc tacagagccc gagactctgt ctcaaaaaac aaaaaaaaca aaaaaaaaca 1080
aaaaaaaaat tagctgggcc tgatggcacg tgcctgtagt cccagctact caggaggctg 1140
aggcaagaga attgcttgaa cctgggaggt ggaggttgca gtgagccgag attgcaccac 1200
tgcattctag cctggcgaca gagcgagact tcgtctcaaa acaaaaacaa gcaaacaaaa 1260
aaaaaaaaaa aaaaaaaaaa 1280

<210> 6
<211> 58
<212> PRT
<213> Homo sapiens

<400> 6
Met Glu Asn Glu Leu Ile Ala Leu Gly Ala Ser Phe Arg Asp Val Thr
1 5 10 15

Ala Ala Ser Thr His Cys Ile Cys Asp Lys Ala Asp Thr Arg Asp Asn
20 25 30

Arg Gly Tyr Val Phe Leu Lys Met Tyr Leu Val Lys Glu Lys Asn Pro
35 40 45

Leu Phe Ile Tyr Asp Gly Lys Leu Gly Thr
50 55

<210> 7
<211> 1001
<212> DNA
<213> Homo sapiens

<400> 7
aggattgggc ttcaatgtga ctaacctaca attgcctcca ggtgctccac ccactgagtc 60
cttgtgtctc tgctgaggtc cttggagagt tactggagag ggctctgtgt cagatgacct 120
tgaggaggct ctgatttagc cttttgtaaa atgcaaagag ttgaggtctt ctccacgcaa 180
gagctcgctg atgtcaatga ggtattgagg atggggccat ctcctatttc tgtggccagt 240
actgagtttt gttatccttc ctttaggtaa ggagtgccaa tggaccgatg cctgcctgtc 300
tcatccctgt gcaaatggaa gtacctgtac cactgtggcc aaccagttct cctgcaaatg 360
cctcacaggc ttcacagggc agaagtgtga gactgatgtc aatgagtgtg acattccagg 420

acactgccag catggtggca cctgcctcaa cctgcctggt tcctaccagt gccagtgcct 480
tcagggcttc acaggccagt actgtgacag cctgtatgtg ccctgtgcac cctcgccttg 540
tgtcaatgga ggcacctgtc ggcagactgg tgacttcact tttgagtgca actgccttcc 600
aggtaaggag ctccctagtg tcccaggatt aggggacaaa cccctagcac aggaggtagt 660
gggtgtggct caattgtttt ttttaggaag cgcaaggaaa aagggaagtg agaattttgt 720
ggggggtggg ttgctagtga gggaggagtt ttatgggccc actgtggtcc ataaactgag 780
caggggataa tttagcatgt cagggtttat gatgatgagt ggctagaaaa ttgtttattg 840
tccctttgt agaaacagtg agaagaggaa cagagctctg ggaaagagac agggaagtct 900
ggaatggaaa agaacacgat gagaattaga cactggaaaa tatgtatgtg tggttaataa 960
agtgctttaa actgaaaaaa aaaaaaaaaa aaaaaaaaaa a 1001

<210> 8
<211> 114
<212> PRT
<213> Homo sapiens

<400> 8
Met Pro Ala Cys Leu Ile Pro Val Gln Met Glu Val Pro Val Pro Leu
1 5 10 15

Trp Pro Thr Ser Ser Pro Ala Asn Ala Ser Gln Ala Ser Gln Gly Arg
20 25 30

Ser Val Arg Leu Met Ser Met Ser Val Thr Phe Gln Asp Thr Ala Ser
35 40 45

Met Val Ala Pro Ala Ser Thr Cys Leu Val Pro Thr Ser Ala Ser Ala
50 55 60

Phe Arg Ala Ser Gln Ala Ser Thr Val Thr Ala Cys Met Cys Pro Val
65 70 75 80

His Pro Arg Leu Val Ser Met Glu Ala Pro Val Gly Arg Leu Val Thr
85 90 95

Ser Leu Leu Ser Ala Thr Ala Phe Gln Val Arg Ser Ser Leu Val Ser
100 105 110

Gln Asp

<210> 9
<211> 2058
<212> DNA
<213> Homo sapiens

<400> 9
tttttatat atgacctttg atttctgttg tttgtatttt agcacagtgt atgcaccttc 60
atttaaatac atctgtgtgc atacagatac gcatatatgt gtgtgcgtat gcatatatct 120
ctcatctgta gtttccaaga gttcagctga agcagatgga gtcctgcagc ccaggagaca 180
ccctgcatcc ctgctaatag tgtttgccac aagtattagt gagtcttcct tattaatatt 240
ttcatttcag aagactgaag caaagctgat agtgtttgct gtttctttgg cagctaagtg 300
agggtcttgg gatgacttgc tgtgttcctc aagctgcact ttggggccat ctctgcagta 360
ttagcccccct ttttgcttgg tggtactctg tctgtgcctg tgtgtgtgtg tgatagtcac 420
tcttgcatgg cttccatgtc tggtttgtgg catttgggga taaggtgctg aagccagagc 480
atttgcagtt tgtttgaggc ctcgttgcca atgatagatc actcctgttg acctggtatg 540
tctgcttgct tgctgctttt ccttgctttc tcttggaaga ggaaaggact ctggtcaggc 600
ccaggctgag tgagatgagc tgcagctggc tcatggcctt cttagagcag agagaggagt 660
atgtcatttt actaagttcc taaacaaaca tttatgcagg caacactcct tgcagatcca 720

gaaactgagg cacaataggg ttatgacttg ctcaagaata tgtagctgct agggggtaaa 780
tcaaggcatc acaatttctg ttcagcgggc aggaataggc tgtgaattgc tagcactttt 840
ttttttaag caattacttt ttgacttgtt cctctgaaag tgcaagaggc gtacaccttt 900
cccaaatgta gactagaatc tgcaggatgc cacccactgt atagttctgc tttcccagag 960
aggaagaact tttagaaacc aaatgatctt aattgttatt gcccacccct ggcttttccg 1020
ggtagaaaat tcacagtagg aatgattgtt aagagagagt gcttggaacc atgggttaac 1080
aggaaaggct acctaacttc acatatctgc aaccagagca gccaccaagc attacttagc 1140
agcaggaaaa tgattgtatt tgagttcctg tgtgtccaaa actgaggcac catgttcttt 1200
gaaaacatgc cacctcaagg ctgggcgcgg tggctcacac ctgtaatccc agcactttgg 1260
gaggccgagg cgggcggatc accggaggtc gggagtttga gaccagcctg accaacatgg 1320
agaaacccca tctctactaa aaatacaaaa ttagccgggc gtggtggcat gcgcctataa 1380
tctcagctac ttgggaggct gaggcaggag aattgcttga acccaggagg cggaggttgc 1440
ggtgagttga gatcgtgcca ttgcactccg gcctgggcaa caacagcaaa actccgtctc 1500
aaaaaaaaaa aaaaaaaaaa tgccacctca cagtctctat cgttgggccc tgtggttgca 1560
aagctgcctc ctgaattaag aaggaaaggg aaaagatata gctggaagcg agtggaagag 1620
atgctgaggg ctggggctgc acagacgtgc tcagcagggc tacaggtgct caagccctat 1680
tggggatggg tggggagtgg ggcagcggcg tttgccacct taagaattgg ggccaaagcc 1740
actgatgttt atttgacagt gacactgcac tggtacttta aagaaattat ttccccttgt 1800
aattataatt actgcttatt aaggaaaata tgggaatttt agaaagaatc aagtttgcca 1860
cccaaatgct accactgtta atcttttggt gttaaatgtt ccccctagac atttctgtgc 1920
atagattttt ggtgtgttta catagtcgtt attctgtata tacaatttta tgtccctttt 1980
gtacttaacg tataaacatt ttttccatgt taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040
aaaaaaaaaa aaaaaaa 2058

<210> 10
<211> 96
<212> PRT
<213> Homo sapiens

<400> 10
Met Thr Phe Asp Phe Cys Cys Leu Tyr Phe Ser Thr Val Tyr Ala Pro
1 5 10 15

Ser Phe Lys Tyr Ile Cys Val His Thr Asp Thr His Ile Cys Val Cys
20 25 30

Val Cys Ile Tyr Leu Ser Ser Val Val Ser Lys Ser Ser Ala Glu Ala
35 40 45

Asp Gly Val Leu Gln Pro Arg Arg His Pro Ala Ser Leu Leu Ile Val
50 55 60

Phe Ala Thr Ser Ile Ser Glu Ser Ser Leu Leu Ile Phe Ser Phe Gln
65 70 75 80

Lys Thr Glu Ala Lys Leu Ile Val Phe Ala Val Ser Leu Ala Ala Lys
85 90 95

<210> 11
<211> 1498
<212> DNA
<213> Homo sapiens

<400> 11
ggacttcctc taccatcctc gggtggacat tttgtttgct tttccattaa tccactggtt 60
tagtttccag aacgcaatgt cagacctgag gtgacagaaa agggaaaacg tgagagagtg 120
tcttcttccc tgaagagagg tgggcctgag gcttgacagt ggcgctgcct gagtgaccta 180
gccgctgggc tgggccctgg acagctgatc ccaggttcct gcacttgtcg ccacccttcc 240
gtagtccaca ggcctgatgg cggcggcggc tgagccgatg ggcccggcac aggttcccat 300

gaactcagaa gtaattgtgg accctataca ggggcaggtg aactttgagg acgtgttcgt 360
gtacttctcc caggaggagt gggtgctcct tgatgaggct cagaggctcc tgtaccgtga 420
tgtgatgctg gagaactttg cacttatggc ctctctgggg atacctcaga caatggcagc 480
ttttggattg aaatatttgc tgaatgacac tggatacaca agcagcaagt ccaacacaat 540
cacagcaaca gactctcctg cagaccttcc caggaagaca gagccacaca caccatcatg 600
gtcctggtga gctccttttt tgttttctat tcagtccata gttttctgac aatttggaca 660
actgtagttg caaacccagg ccagtggata gtgaccaact ctgtgttggt cgcctcatgt 720
ttcccagcac gcagcccttt tgtcctcatc atgagtgata ctcatatctc tcagttctgt 780
tttgcctgca ggacaaggaa aacactcttt cctaatctgg ttgtcatgcc atgagtcttt 840
tctcttcatg gaattcagct atttatcata actcttgcta agatttagga aatattaact 900
actagttatt tgtgatagca acatacacat ggccagtaat gctcttgtcc aggaagatct 960
aataccagag ctaaaaatga aagtcatgga tactgttaca caaagaacac tctatataac 1020
tgtgttaagt ccttcagaca agttcaggaa atcaaaaagt ttaaaaaggg aattctttag 1080
agatttaggg gagatttctc atttttgtac tatgaagaat catggaatgt tttaaaaata 1140
tttttaaagc acagtttgat tcaggtgctt cttgaacagc ataaatcccc tggagagtcc 1200
acatgtaaga aagacatgtg caggccgggc acagtggctc acgcctgtaa tcccaccgtt 1260
ttgggaggct gaggcactcc caaatgcctc aagtgatcca ctcaagatga cttgaggcca 1320
ggagttcgag accagcctgg ccaacatggc aaaaaccctg tctcaaatac aaaaattagc 1380
caaccatgtg gcacacacct gtagtcccag ctactccaga gggtgaagca cgagaattac 1440
ttaccagctt gggtgacgga gggagactca aaaaaaaaaa aaaaaaaaaa aaaaaaa 1498

<210> 12
<211> 117
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Ala Ala Ala Glu Pro Met Gly Pro Ala Gln Val Pro Met Asn
1 5 10 15

Ser Glu Val Ile Val Asp Pro Ile Gln Gly Gln Val Asn Phe Glu Asp
20 25 30

Val Phe Val Tyr Phe Ser Gln Glu Glu Trp Val Leu Leu Asp Glu Ala
35 40 45

Gln Arg Leu Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Ala Leu Met
50 55 60

Ala Ser Leu Gly Ile Pro Gln Thr Met Ala Ala Phe Gly Leu Lys Tyr
65 70 75 80

Leu Leu Asn Asp Thr Gly Tyr Thr Ser Ser Lys Ser Asn Thr Ile Thr
85 90 95

Ala Thr Asp Ser Pro Ala Asp Leu Pro Arg Lys Thr Glu Pro His Thr
100 105 110

Pro Ser Trp Ser Trp
115

<210> 13
<211> 1718
<212> DNA
<213> Homo sapiens

<400> 13
ttctgcctct cgctggaggc caggccgtgc agcatcgaag acaggaggaa ctggagcctc 60
attggccggc ccggggcgcc ggcctcgggc ttaaatagga gctccgggct ctggctggga 120

cccgaccgct gccggccgcg ctcccgctgc tcctgccggg tgatggaaaa ccccagcccg 180
gccgccgccc tgggcaaggc cctctgcgct ctcctcctgg ccactctcgg cgccgccggc 240
cagcctcttg ggggagagtc catctgttcc gccggagccc cggccaaata cagcatcacc 300
ttcacgggca agtggagcca gacggcttcc ccaagcagta ccccctgttc cgccccccctg 360
cgcagtggtc ttcgctgctg gggccgcgc atagctccga ctacagcatg tggaggaaga 420
accagtacgt cagtaacggg ctgcgcgact ttgcggagcg cggcgaggcc tgggcgctga 480
tgaaggagat cgaggcggcg ggggaggcgc tgcagagcgt gcacgcggtg ttttcggcgc 540
ccgccgtccc cagcggcacc gggcagacgt cggcggagct ggaggtgcag cgcaggcact 600
cgctggtctc gtttgtggtg cgcatcgtgc ccagccccga ctggttcgtg ggcgtggaca 660
gcctggacct gtgcgacggg gaccgttggc gggaacaggc ggcgctggac ctgtacccct 720
acgacgccgg gacggacagc ggcttcacct tctcctcccc caacttcgcc accatcccgc 780
aggacacggt gaccgagata acgtcctcct ctcccagcca cccggccaac tccttctact 840
acccgcggct gaaggccctg cctcccatcg ccagggtgac actggtgcgg ctgcgacaga 900
gccccagggc cttcatccct cccgccccag tcctgcccag cagggacaat gagattgtag 960
acagcgcctc agttccagaa acgccgctgg actgcgaggt ctccctgtgg tcgtcctggg 1020
gactgtgcgg aggccactgt gggaggctcg ggaccaagag caggactcgc tacgtccggg 1080
tccagcccgc caacaacggg agcccctgcc ccgagctcga agaagaggct gagtgcgtcc 1140
ctgataactg cgtctaagac cagagccccg cagcccctgg ggcccccggg agccatgggg 1200
tgtcgggggc tcctgtgcag gctcatgctg caggcggccg agggcacagg gggtttcgcg 1260
ctgctcctga ccgcggtgag gccgcgccga ccatctctgc actgaagggc cctctggtgg 1320
ccggcacggg cattgggaaa cagcctcctc ctttcccaac cttgcttctt aggggccccc 1380
gtgtcccgtc tgctctcagc ctcctcctcc tgcaggataa agtcatcccc aaggctccag 1440
ctactctaaa ttatgtctcc ttataagtta ttgctgctcc aggagattgt ccttcatcgt 1500
ccaggggcct ggctcccacg tggttgcaga tacctcagac ctggtgctct aggctgtgct 1560
gagcccactc tcccgagggc gcatccaagc gggggccact tgagaagtga ataaatgggg 1620
cggtttcgga agcgtcagtg tttccatgtt atggatctct ctgcgtttga ataaagacta 1680
tctctgttgc tcacaaaaaa aaaaaaaaaa aaaaaaa 1718

<210> 14
<211> 105
<212> PRT
<213> Homo sapiens

<400> 14
Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala
1 5 10 15

Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu
20 25 30

Ser Ile Cys Ser Ala Gly Ala Pro Ala Lys Tyr Ser Ile Thr Phe Thr
35 40 45

Gly Lys Trp Ser Gln Thr Ala Ser Pro Ser Ser Thr Pro Cys Ser Ala
50 55 60

Pro Leu Arg Ser Gly Leu Arg Cys Trp Gly Pro Arg Ile Ala Pro Thr
65 70 75 80

Thr Ala Cys Gly Gly Arg Thr Ser Thr Ser Val Thr Gly Cys Ala Thr
85 90 95

Leu Arg Ser Ala Ala Arg Pro Gly Arg
100 105

<210> 15
<211> 847
<212> DNA
<213> Homo sapiens

<400> 15
acacacacat ctgcacctca accacagact acacttgctg aactggctcc tggggccatg 60
aggctgtcac tgccactgct gctgctgctg ctgggagcct gggccatccc agggggcctc 120
ggggacaggg cgccactcac agccacagcc ccacaactgg atgatgagga gatgtactca 180
gcccacatgc ccgctcacct gcgctgtgat gcctgcagag ctgtggctta ccagatgtgg 240
caaaatctgg caaaggcaga gaccaaactt catacctcaa actctggggg gcggcgggag 300
ctgagcgagt tggtctacac ggatgtcctg gaccggagct gctcccggaa ctggcaggac 360
tacggagttc gagaagtgga ccaagtgaaa cgtctcacag gcccaggact tagcgagggg 420
ccagagccaa gcatcagcgt gatggtcaca gggggcccct ggcctaccag gctctccagg 480
acatgtttgc actacttggg ggagtttgga gaagaccaga tctatgaagc ccaccaacaa 540
ggccgagggg ctctggaggc attgctatgt gggggacccc agggggcctg ctcagagaag 600
gtgtcagcca caagagaaga gctctagtcc tggactctac cctcctctga aagaagctgg 660
ggcttgctct gacggtctcc actcccgtct gcaggcagcc aggagggcag gaagcccttg 720
ctctgtgctg ccatcctgcc tccctcctcc agcctcaggg cactcgggcc tgggtgggag 780
tcaacgcctt cccctctgga ctcaaataaa acccagtgac ctcaaaaaaa aaaaaaaaaa 840
aaaaaaa 847

<210> 16
<211> 189
<212> PRT
<213> Homo sapiens

<400> 16
Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
1 5 10 15

Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
20 25 30

Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
35 40 45

Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
50 55 60

Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
65 70 75 80

Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
85 90 95

Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
100 105 110

Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
115 120 125

Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
130 135 140

His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
145 150 155 160

Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
165 170 175

Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
180 185

<210> 17
<211> 1448
<212> DNA
<213> Homo sapiens

<400> 17
atttcatccc tgcgctgtcc tagcaccctg tcgctggagt tggcatgcag agactttgtc 60
aggatgggag aggccgcagt gtatcggatc tgtcgttctg gaaagaagac ccttctattt 120
agagtagaaa caaacgaaac ttctaaggta tcatctgtgt taagtgatga gaccatattt 180
ctttgatgtt tctgaacatc aaagctgatt cagtactggt agatgtgctc attctccctg 240
aaacataccc atcatatttc ctattataat tacatctcat tgtcctgtgg aggtggacat 300
gataaacatt atcttttgtt ttcttgtttt gttttgtttg agacggtctc attctgtcac 360
ccagactgga gtgcagtgcc acaatcatgg ctcaccgcat tgacctcctt ggctcaaggc 420
atcctcccac ctcagcttcc tgactagctg ggactactgg tgtgcaccac cacacccagc 480
taattttcaa tttttcatag agacagggtc tcactgtgtt gtccaggctg gtcttgaact 540
cctgggctca agccacccgc ccacctgggc ctcccaaagt gctgggatta caggcatcag 600
ccatcacacc catccataaa cattatatta atgtcacatt acaaaactga gacctaagtt 660
gcttaggata aaatgaaatt gaaagactag ctaacatgaa aatttatatt ttggcttttt 720
catgtttttt gataaaacca gtgtatttga atgattcttt tgatgtttag taatggtttt 780
ttgtttgttt tttggttttt ttttttgag acggagtctc actctgtcgc cagtctggag 840
tgctagtggc gcgatcttgg cttactgcag cctccacttc ccaagttcaa gcgattctcc 900
tgcctcagcc tcccgagtag ctgggactac aggcgcatgc caccacgccc ggctaatttt 960
tgtattttta gtagagacgg agtttcactg tgttggccag gatggtctcg atctcgacct 1020
cgtgatcacc caccttggcc tctcaaagtg ctgggattac aggcgtgagc caccacgcct 1080
ggcctatgtt taataatgtt gaaataggat ggaatatttt gttaaattaa cattttaaaa 1140
ttagaagaca ccgttttaat ttttaaaccc ttcctcctct cattgtaacg aaattaattc 1200
cagctgcagt gagaaaactt aaaaatcatg atacaaaatg aaacaatatc tgaaagtagt 1260
tttataaaac tgaaattgct gttaaagaga atgtgttagt gacttaacca tttgctctat 1320
gtgatgttta ttatcaaata catataattt tgaagatttt aatgaatggc ttaagatttt 1380
atctttgtgt agaatgtggc taaagaaacc ttagttgaga ttcaaaaaaa aaaaaaaaaa 1440
aaaaaaaa 1448

<210> 18
<211> 106
<212> PRT
<213> Homo sapiens

<400> 18
Met Val Phe Cys Leu Phe Phe Gly Phe Phe Phe Leu Arg Arg Ser Leu
1 5 10 15

Thr Leu Ser Pro Val Trp Ser Ala Ser Gly Ala Ile Leu Ala Tyr Cys
20 25 30

Ser Leu His Phe Pro Ser Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg
35 40 45

Val Ala Gly Thr Thr Gly Ala Cys His His Ala Arg Leu Ile Phe Val
50 55 60

Phe Leu Val Glu Thr Glu Phe His Cys Val Gly Gln Asp Gly Leu Asp
65 70 75 80

Leu Asp Leu Val Ile Thr His Leu Gly Leu Ser Lys Cys Trp Asp Tyr
85 90 95

Arg Arg Glu Pro Pro Arg Leu Ala Tyr Val
100 105

<210> 19
<211> 2166
<212> DNA
<213> Homo sapiens

<400> 19
atgattttg gagcttgctt cctcattgac ttcatgtatt ttgaaagatc tccaccacaa 60
cgttcaagat agagagacac agcaagccat caactatggt taattttgaa aaatggaaaa 120
gttggattgg gcttacagtc agcactcagt tatttgcaag tgtatttctt tgctttgtag 180
agtattttta ttgggtgtta actttgacag ctgagagtgg gcttgcaaga acacaatcta 240
aaagtgtgtt tcaattgagt atctctctag tagaatagga gttcatcctg aaaagctgtg 300
actcattaac ccagtaaaca tatacaaagt aagcttaaaa cactataaac atgagataag 360
ggaaaatgaa tccagagttc tcatattaat aggtagtgaa acaataaggc tttttagagc 420
agactttgtt ggcataaaat aacctggctt ctatccctaa ccctttccta cctttcctct 480
ccgtcaacat gtcctcatac tgaagacaaa cttgtttcaa tgatagtctt cattttcaaa 540
aacaaaaagg caggcagaca gaaataatga tgtttttcttg cactaagaag gtactacttg 600
tacacatata tcaaaacctc attctgcaaa gtttttgaag gtttcaatgg gaaatttgat 660
tttattacaa aataaaacat tttttaatgt taaagtttat atattccatg cttgttttct 720
cattcactgg catggatgat caggagctgc ctatatatga aggcagaatc agactatcag 780
gaaaggagct ggccagggcc acagccagtc aagatctctg agcaacttag agacattggt 840
gtcattatat gaagcttgca tttaatacat ttatacataa tacatttgta catttaattc 900
ataacgtctc ttggtcacag atgccttata tataaaataa gttgccagat ctctaagatt 960
gcctagtaca cctttgtatc tcatttgatg tgatacccag aagagatcat tgttttttgt 1020
ttttgttttt gtttttttca agaagatcct tcgtgatcac catgctgttc tcatggtaag 1080
aactggagtt atgtttttaa atttggaaat atgacatttt atgtagcact ttataaaaag 1140
tgaaagcgac aaattccacc gctgcttaat actgctttgc ttctttttat tgacatgata 1200
gataaatatg tatctacaca gagtaataat aataaaacac agtaaacatt ctatttctct 1260
atggtctaca gcatgccagt aaataatatg taggaccaat aataaattat caattacaca 1320
tttttgtgtt aactaattaa aagcatagtg tataagtgag tacactctaa ttaacttgct 1380
tctgttgcac tttagttttc tacctgcata tggactgcat tttttttttt aacacagtca 1440
gtatgtagaa tgggatgtat tcttctgctg ctgcttatta aataaagaaa gcctgagtgt 1500
tcttagatgg ggttattctg agatgagggt cttagcctac agttcttttt gaaatgaaag 1560
gtgctttgtt ttttaattat attcatcttt tcagggtaaa tttgttttttc tgagtttctc 1620
gtaatgctca tttttacatg ctgctactag cttttttttt taaaaaaagt aaaagttgct 1680
gctttctaaa atattaattg ccttatattt gaaagtgcca ttgcaatcgt aagtagacta 1740
tgtatttcct ataatgatgt ctgatattta aataggaaat cagacaaaca atattcagaa 1800
agtttaagca tataaacttt ttatttttaa cttgcctaaa tccctgtatt ccaaaacctg 1860
ctgcatcata ataaatatat ctatatatat ttagcataag acgtgatatt tttaatttct 1920
tttttaaaaa attatatttg tctcttagag ttaaaatttt ctttatataa tattgtcata 1980
tgtcatagtt ttaatacaat tcacatgatt tctatgtttc ttaatgatat tttgttgtgt 2040
aaaattgatc ggattgatta aaaaacaaat tctctggaat ttgtgcgttc atgctttttc 2100
gtattcttta tggcttttaa ataaatatac aatggttaat agtaaaaaaa aaaaaaaaaa 2160
aaaaaa 2166

<210> 20
<211> 60
<212> PRT
<213> Homo sapiens

<400> 20
Met Val Asn Phe Glu Lys Trp Lys Ser Trp Ile Gly Leu Thr Val Ser
1 5 10 15

Thr Gln Leu Phe Ala Ser Val Phe Leu Cys Phe Val Glu Tyr Phe Tyr
20 25 30

Trp Val Leu Thr Leu Thr Ala Glu Ser Gly Leu Ala Arg Thr Gln Ser
35 40 45

Lys Ser Val Phe Gln Leu Ser Ile Ser Leu Val Glu
50 55 60

<210> 21
<211> 1833
<212> DNA
<213> Homo sapiens

<400> 21
gtgtgtgtaa tatcaacgca gtgtatttaa tttggggaag tcactaggtt agaactgtag 60
gcatactcag tggagaggaa gctacctatt ctattctaac tattctgagg tcttcctgga 120
gagggattgt tttagcagct cctctccaga gggggctgga agtccagttt caccaatgac 180
caagttttat ttccttgtcc ttgttttagt tttttcattt tgttttcagt ccaggtgcct 240
cgcagctctt ttggaatggg ccagcattag tctaatttta agcgctatgt gttttgtacc 300
cttgcaaact tgctttctct ttcttcttgc tgttgccctt tgaatgaagc cttgtgtgct 360
tgcatgatca gaccctgtaa taggatgaat ttccatgcac ttaacatgaa gagatacaaa 420
aagaatctag agagagatat atatttttaa tgaaatagaa gcttggcata gaaacattga 480
tttagatgtt atgagttgct ggccagagat tcctcagata aaagagccta gaaaattgag 540
ttttgagcgg gcatggtggc tcacgcctgt aatgccagta gtttgggagg ctgaggcggg 600
tggatcacct gaggtcagga gttcgagatc agcctggcca acatggtgaa accccgcctc 660
tactaaaaaa tatgcaaaat tagccgggcg tggtggtgca ggcctgtaat cccagctact 720
cagaggctga ggcaggagat tcacttgagc ccaggaggtg gaggttgcag tgagccaaga 780
tcgcgccatt gcactccagt cagggcaaca agagtgaaac tccgtctcaa aatataaaag 840
aaaattgagt gtcccaccca aatttaggg cgtacctcct tccatttgat aagaagatgc 900
tatttccagt gtccctggga gaattcttcc atccagttta tatggtgaat tgccaccagc 960
gttccctaaa ggaagagaga acttagctta tttctgtctg tgacttttat cagctagatc 1020
agttaattgt atttttaaat taaaaattag taactagagg aagagactaa gagaactatt 1080
tttacctgag taaatgctct cctcttcttg tgtccaaatc taatgcagag gtgaaaacac 1140
ttgatgagaa aatcctttgt ggcttgaggg gaatcatgtt tctttcagga cgtgttgttt 1200
ccctgaagtc tatgtcacac tgagaacttt ttctgactgc actgctttgg agctattcat 1260
ttaaattgag tttggcctag ttttcctggt ataaaacagg aaatctacat tgttccctct 1320
ttctctccct tccatccctt cccctgcctt tcctatacac gctggtgtgc ttttgccctc 1380
agaaattctt ggtttgggag ttatgtattt ttgagtgatc gaggttatga catacttgga 1440
gcggcatgat ttcaagaagc cattccaaat tcttatagct ccttagctct ggttttactc 1500
tcgtattttc cccaagaaaa ttttttggct attcaaagaa agcacaaaat atgtgatgtg 1560
gaactcatga aaatagggac ttttgatatc tctttaaata ttccctgact cacggaaaag 1620
atgtcctctt ttggtgtata cattgtgaaa atctacccat ttatctctct ctctctcttt 1680
tcttttaaat aaattatctg ataaggccgg caaggtggct cacgcctgta atcccagcac 1740
tttgggaggc cgaggcgagc ggatcacgag gtcaggagat cgagaccgcg gtgaaacccc 1800
gtctctacta aaaaaaaaaa aaaaaaaaaa aaa 1833

<210> 22
<211> 55
<212> PRT
<213> Homo sapiens

<400> 22
Met Thr Lys Phe Tyr Phe Leu Val Leu Val Leu Val Phe Ser Phe Cys
1 5 10 15

Phe Gln Ser Arg Cys Leu Ala Ala Leu Leu Glu Trp Ala Ser Ile Ser
20 25 30

Leu Ile Leu Ser Ala Met Cys Phe Val Pro Leu Gln Thr Cys Phe Leu
35 40 45

Phe Leu Leu Ala Val Ala Leu
50 55

<210> 23
<211> 1504
<212> DNA
<213> Homo sapiens

<400> 23
tctcattgct ggcattgcca ttcctgccat ggtcattggc attcctgttt atgttggaag 60
gaagattcac agcaggtatg agggaaggaa aacctccaaa cacaagagga atttggctat 120
cactggagga gtgactttgt cggtcattgc atccccagtt attgctgcag ttagtgttgg 180
tattggtgtc cccattatgc tggcatatgt ttatggggtt gtgcccattt ctctttgtcg 240
tggaggcggc tgtggagtta gcacagccaa cggaaaagga gtgaaaattg aatttgatga 300
agatgatggt ccaatcacag tggcagatgc ctggagagcc ctcaagaatc ccagcattgg 360
ggaaagcagc attgaaggcc tgactagtgt attgagcact agtggaagcc ctacagatgg 420
acttagtgtt atgcaaggtc cttacagcga aacggccagc tttgcagccc tctcaggggg 480
cacgctgagt ggcggcattc tctccagtgg caagggaaaa tatagcaggt tagaagttca 540
agccgatgtc caaaaggaaa ttttccccaa agacacagcc agtcttggtg caattagtga 600
caacgcaagc actcgtgcta tggccggttc cataatcagt tcctacaacc cacaggacag 660
agaatgcaac aatatggaaa tccaagtgga cattgaagcc aaaccaagcc actatcagct 720
ggtgagtgga agcagcacgg aggactcgct ccatgttcat gctcagatgg cagagaatga 780
agaagaaggt agtggtggcg gaggcagtga agaggatccc ccctgcagac accaaagctg 840
tgaacagaaa gactgcctgg ccagcaaacc ttgggacatc agcctggccc agcctgaaag 900
catccgcagt gacctagaga gttctgatgc acagtcagac gatgtgccag acatcacctc 960
agatgagtgt ggctcccccc gctcccatac tgcagcctgc ccctcgaccc ccagagccca 1020
aggtgcaccg agcccaagtg cccatatgaa cctctctgcc ctagccgagg gacaaactgt 1080
cttgaagcca gaaggtggag aagccagagt atgaagtgga atgaatgctc ctgttctgag 1140
aagcacactt gtaactgcat cttttggaat tttttttttt ttttttccaa ggggtagaga 1200
tttatgtatt ttatttcaca gattctctgg tcacaggttt ttgcccaggg aaattctgag 1260
aaattcacaa tttcttacca gataaaacat gaaaagtttg ccgttagttc ccctcccctc 1320
ccctccctct ttttagtttt aatttattgg ttaaactgat ggcagcaatc catgaggtgt 1380
gtcaaagagt gtacatatgt atgtgtgtat attgaatgct aaacatatta ctgaaagaca 1440
cattttaata aagatttctg tcataattca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaa 1504

<210> 24
<211> 361
<212> PRT
<213> Homo sapiens

<400> 24
Met Val Ile Gly Ile Pro Val Tyr Val Gly Arg Lys Ile His Ser Arg
1 5 10 15

Tyr Glu Gly Arg Lys Thr Ser Lys His Lys Arg Asn Leu Ala Ile Thr
20 25 30

Gly Gly Val Thr Leu Ser Val Ile Ala Ser Pro Val Ile Ala Ala Val
35 40 45

Ser Val Gly Ile Gly Val Pro Ile Met Leu Ala Tyr Val Tyr Gly Val
50 55 60

Val Pro Ile Ser Leu Cys Arg Gly Gly Gly Cys Gly Val Ser Thr Ala
65 70 75 80

Asn Gly Lys Gly Val Lys Ile Glu Phe Asp Glu Asp Asp Gly Pro Ile
85 90 95

Thr Val Ala Asp Ala Trp Arg Ala Leu Lys Asn Pro Ser Ile Gly Glu
100 105 110

Ser Ser Ile Glu Gly Leu Thr Ser Val Leu Ser Thr Ser Gly Ser Pro
115 120 125

Thr Asp Gly Leu Ser Val Met Gln Gly Pro Tyr Ser Glu Thr Ala Ser
130 135 140

Phe Ala Ala Leu Ser Gly Gly Thr Leu Ser Gly Gly Ile Leu Ser Ser
145 150 155 160

Gly Lys Gly Lys Tyr Ser Arg Leu Glu Val Gln Ala Asp Val Gln Lys
165 170 175

Glu Ile Phe Pro Lys Asp Thr Ala Ser Leu Gly Ala Ile Ser Asp Asn
180 185 190

Ala Ser Thr Arg Ala Met Ala Gly Ser Ile Ile Ser Ser Tyr Asn Pro
195 200 205

Gln Asp Arg Glu Cys Asn Asn Met Glu Ile Gln Val Asp Ile Glu Ala
210 215 220

Lys Pro Ser His Tyr Gln Leu Val Ser Gly Ser Ser Thr Glu Asp Ser
225 230 235 240

Leu His Val His Ala Gln Met Ala Glu Asn Glu Glu Glu Gly Ser Gly
245 250 255

Gly Gly Gly Ser Glu Glu Asp Pro Pro Cys Arg His Gln Ser Cys Glu
260 265 270

Gln Lys Asp Cys Leu Ala Ser Lys Pro Trp Asp Ile Ser Leu Ala Gln
275 280 285

Pro Glu Ser Ile Arg Ser Asp Leu Glu Ser Ser Asp Ala Gln Ser Asp
290 295 300

Asp Val Pro Asp Ile Thr Ser Asp Glu Cys Gly Ser Pro Arg Ser His
305 310 315 320

Thr Ala Ala Cys Pro Ser Thr Pro Arg Ala Gln Gly Ala Pro Ser Pro
325 330 335

Ser Ala His Met Asn Leu Ser Ala Leu Ala Glu Gly Gln Thr Val Leu
340 345 350

Lys Pro Glu Gly Gly Glu Ala Arg Val
355 360

<210> 25
<211> 2350
<212> DNA
<213> Homo sapiens

<400> 25
agtcccgtag taatgtacca tcagcttctg aagttcctga taatagggca tctgaagctt 60
ctcagggatt tcgatttctt aggcgaagat ggggtttgtc atctcttagc cacaatcata 120
gctctgagtc agattcagaa aattttaacc aagaatctga aggtagaaat acaggaccat 180
ggttatcttc ctcacttaga aatagatgca cacctttgtt ctctagaagg aggcgagagg 240

```
gaagagatga atcttcaagg atacctacct ctgatacatc atctagatct catattttta 300
gaagagaatc aaatgaagtg gttcaccttg aagcacagaa tgatcctctt ggagctgctg 360
ccaacagacc acaagcatct gcagcatcaa gcagtgccac aacaggtggc tctacatcag 420
attcggctca aggtggaaga aatacaggaa tatcagggat tcttcctggt tccttattcc 480
ggtttgcagt ccccccagca cttgggagta atttgaccga caatgtcatg atcacagtag 540
atattattcc ttcaggttgg aattcagctg atggtaaaag tgataaaact aaaagtgcgc 600
cttcaagaga tccagaaaga ttgcagaaaa taaaagagag cctcctttta gaggactcag 660
aagaagaaga aggtgactta tgtagaattt gtcaaatggc agctgcatca tcatctaatt 720
tgctgataga gccatgcaag tgcacaggaa gtttgcagta tgtccaccaa gactgtatga 780
aaaagtggtt acaggccaaa attaactctg gttcttcatt agaagctgta accacctgtg 840
aactatgtaa agagaagttg gagcttaacc tggaggattt tgatattcat gaactacata 900
gagctcatgc aaatgaacaa gctgagtatg agtttatcag ctctggtctc tacctagtgg 960
tgttattgca cttgtgcgaa caaagctttt ctgatatgat gggaaataca aatgaaccaa 1020
gcacacgtgt ccgacttcag aggatgattc cgaagaagac ggagaccata acaggacatt 1080
tgatattgcc taacttcata taagacagat ggatgatctg tgaacataag tgtttattaa 1140
aaatggcaat taaatataaa ttacttttgt gggggaatgc ctaataaata cattgactat 1200
atataaaatg aatatataca tacacatgta tgcctgtata tatatattca ttctccagtg 1260
ttgctgaatt aaaattctgc tggacttttt aacatagcaa atccgatgtt tataaactgg 1320
taatcaaaaa ggttttttct tttaggtgag tgggaaagta ttacccttgt tttaaatatc 1380
taagcaatgc ctatcaaccc ttttttgtgt tatgattact gtagtcatat ttatgaaaaa 1440
aggtttgtgt tttactcttg ctagtgagaa aagtgggaca aaatatactt ttgaaataaa 1500
atgctatatg gcacctaatt atttttttctt ttaaaatgcc ttaagttgca gtctcatttt 1560
gataatcatt tgcttccagt gtttaaaaat taaaaaaaga atggggagaa ggttatgaga 1620
agagcattat taagtttcca aatttaattt gaattccaaa ttcacctagc aataaaatct 1680
aatttttaaa aagtatataa atataaaatg tataaatgat ggatagattt ttgtattgat 1740
ttgcaaaatg cagattatat ttgataggct atagtatgta gatattcctt ttaggaatat 1800
tacagctgta aattatatga gacttgccag tcaaatgcta tttggtttaa aaaaattatt 1860
gcaatctcaa gttaatggaa tatttttaaa tcccacattc agagtttaaa acactggttt 1920
tcaatgtgtt ttttagtgtt gtcacttgtt tatagataaa tatataaata acctgtttgg 1980
atcctggtcc tttttaactg ttccttggta attctgagca tttatttgat gacttaatat 2040
ttttcactac ctttggagaa cagatgaaca ttattcacca tgaatggatc tatactgtgt 2100
ggtcatgagt tgtgtatact tccataacac tgtatttttc ttctgtcagt acccttagga 2160
tacactttaa aacaccttaa ggtctgatgt tatggcaaca aactactttt tcaaacctaa 2220
ataggaacca tgtaatttct caaaagtgat tgaacagttt gcccacactt agtttgttgg 2280
tcttatgtaa aacattggct caaaataaag tacacactga tttataaaaa aaaaaaaaaa 2340
aaaaaaaaaa                                                        2350
```

<210> 26
<211> 167
<212> PRT
<213> Homo sapiens

<400> 26

```
Met Tyr His Gln Leu Leu Lys Phe Leu Ile Ile Gly His Leu Lys Leu
  1               5                  10                  15

Leu Arg Asp Phe Asp Phe Leu Gly Glu Asp Gly Val Cys His Leu Leu
             20                  25                  30

Ala Thr Ile Ile Ala Leu Ser Gln Ile Gln Lys Ile Leu Thr Lys Asn
         35                  40                  45

Leu Lys Val Glu Ile Gln Asp His Gly Tyr Leu Pro His Leu Glu Ile
     50                  55                  60

Asp Ala His Leu Cys Ser Leu Glu Gly Gly Glu Arg Glu Glu Met Asn
 65                  70                  75                  80

Leu Gln Gly Tyr Leu Pro Leu Ile His His Leu Asp Leu Ile Phe Leu
                 85                  90                  95
```

Glu Glu Asn Gln Met Lys Trp Phe Thr Leu Lys His Arg Met Ile Leu
100 105 110

Leu Glu Leu Leu Pro Thr Asp His Lys His Leu Gln His Gln Ala Val
115 120 125

Pro Gln Gln Val Ala Leu His Gln Ile Arg Leu Lys Val Glu Glu Ile
130 135 140

Gln Glu Tyr Gln Gly Phe Phe Leu Val Pro Tyr Ser Gly Leu Gln Ser
145 150 155 160

Pro Gln His Leu Gly Val Ile
165

<210> 27
<211> 1635
<212> DNA
<213> Homo sapiens

<400> 27
gaaaatcaca gttgtaaaag cagtctccag ggccaggtat atttagtata gtttttagaa 60
acagcagcca gaaggataat gggaataaaa gttagaagcc tctctctctc tctctctctc 120
tctctctctg tgtgtgtgtg tgtgtgtgtg tgtgtttgtg tttgtatgtt tgtcttgtct 180
ctatcatcca tccctatgtt gattgggaga caggatgctt taatcaagcc ccaggggatc 240
aggggtttag tcttacagca tcctgtgcta acttgctgtg tgaccttaga atatttcttg 300
gcatctctgg gcttcaggcg ctgtctctat acattagtgt gttactgatc ttgtaagtag 360
gaatttagag gcccagggag ggaaagggct tgcttcagtc agttagctta gcctctacac 420
tgagcactct ttaggttgtc tagttttctc cttcttaaat ggaaagaaag aggcctgacc 480
agttcatagg tgcactcttc cttgaaatat aaagcactgc aaatacacaa ggctgaagaa 540
aagaatcaca aagtctttgt gattggtcat agccattttc ataaagcagc agccagactt 600
gccagctaac ttattaccta tggtggaaac ccgttagttc tgaaatgtta cactgttctt 660
tgaccactat ttgagaatta agtgctttgt gattaaaaac aacagcaaca atgctgaatc 720
ttgtaattat ttcataatta agtaaataaa agctgaggtg acctctccgg atttgcaaa 780
gccctgaatg taacttggaa ggggaaaccc attcatttgg cctgaacggg agattacctt 840
gtaggggagc tgctgggtga atatcaaggg tcttttgaag aaaaacagag tagaagagca 900
attgggtaga tacacaagtc aggaaaaatg caaagtgact tagtttgatg cctccaaatg 960
tgtgagttgc tagaaagagg gctcctcact atggctgatc tcctggggggt agaggaaaga 1020
ggagatctga agtaagtgca gtgtaaatag aaggtttgtt acattcttat ttgggagttg 1080
aagccaagtg gaggagtgct gtattttagg agaagtgggc atataaaatg tgatcttaaa 1140
actaaataat ttgagataag ttaattgcag tacaaaaaga tttttacctt actaaaggga 1200
ttcatagtga gtctcctttt aatagctaat tccgttatta tatttcaaat tatttgatga 1260
acacaatcat gatagaccct tttgggagcc tcacctgtta tgcaaaacca aggacttttc 1320
ggttgggcac ggtggctcac ccctgtagtc ccagcacttt gggaggccga ggcaggtgga 1380
tcacgaagtc aagagattga gaccatcctg gccaatatgg tgaaaccccg tgtctactaa 1440
aaatacaaaa aaaaaaatta gctgggcatg gtggcgcgtg cctgtagtcc cagctactcg 1500
ggaggctgag gtaggagaat ggctcgaacc tgtgaggcag aggttgcagt gagttgagat 1560
gccgccactg cactccagcc tggggaaaga gcaagactcc ttctcaaaaa caaaaaaaaa 1620
aaaaaaaaaa aaaaa 1635

<210> 28
<211> 89
<212> PRT
<213> Homo sapiens

<400> 28
Met Gly Ile Lys Val Arg Ser Leu Ser Leu Ser Leu Ser Leu Ser Leu
1 5 10 15

Ser Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Met Phe Val
20 25 30

Leu Ser Leu Ser Ser Ile Pro Met Leu Ile Gly Arg Gln Asp Ala Leu
35 40 45

Ile Lys Pro Gln Gly Ile Arg Gly Leu Val Leu Gln His Pro Val Leu
50 55 60

Thr Cys Cys Val Thr Leu Glu Tyr Phe Leu Ala Ser Leu Gly Phe Arg
65 70 75 80

Arg Cys Leu Tyr Thr Leu Val Cys Tyr
85

<210> 29
<211> 3415
<212> DNA
<213> Homo sapiens

<400> 29
atatacctaa aactgattaa tgttacgggc ctattgaatg tttgtttctg cttgtgtgtt 60
ttcttttttc tatgtttatg aaaatatata catcatcagt tcctctgttc cgagggatgt 120
tgtcatgctt ggcattgtct tgttggtgta gtttgtctgc acccctcagc tcgtgggtta 180
atggtgattg tgggagctgc ctcagtatct ctgacagttc taatgatacg ggaaagtaga 240
actatctgct taggatagat tttaggatta gggttttctg tgtttatgtg aagtattttt 300
atgtgttgag gtataactaa aatcatctaa ggctaaatgt aatgaaacag ctcataacag 360
atgaaatgta catgaataga ttatcctgca gggggagcaa gaggcagacg ggttaaaagt 420
ctgttgggct tttccccaga acaaaacagt aggccttcag gcctgtcact catacagaat 480
gaatcacaag tattttcagg agataagtgt gggtaatatc attcattcgt tgtcattatg 540
gttgccacca agaataggga gctatttaaa tgtatattaa attaataaaa attaaggaaa 600
ccttaaaatt tagctcctca atggcactag tacattctaa gtgtgcaata gccccatgtg 660
tgtggtggtt atattagcaa tacagatacg gagagtttct atcatcgcag aagtctatga 720
aacagtaccg gttttgtcag actgttataa acctttgtgt cttaatgttc gtttattgat 780
ttatttaaac agtggtaata tatagagttt aacaagggga gttatcagtt aacaagttcc 840
tgctcatgca caaagaagaa atcaagtagc ggtgtgatgt tagcttgtaa agaaatcatg 900
gatctgcatt agtaagtcac aggtactcaa ggacccctgg gagtacttgt tttggcagag 960
ttgcctggca gtaagggcac caaaatagct atgggaagga ggcagtttta ctacttctgt 1020
agatcaggaa atggtcttag tgatacttgg acttgttcac agatacttct gttggtagaa 1080
ttcaggactc atgaatattt tagtataagc ctttttttctt cctcagtctg tgtgagcccc 1140
atgcaggact agggaaagtt gtaaggagga cctcggtctc tgtgtgtttc aggagtctct 1200
tggctgatta atcatgttgt tactcatttg gagtaatact aagcccttga agacttcagg 1260
gtggtatacc tggcattgtc cttgatttta aaatatcttg gaatctatta taagaagatt 1320
aggatcatta gcgaaagtac tcattgatgg tcaaaataca ttaaagagct ggaaaaggaa 1380
actgtgaggt gtgatctctc tctctgaatt tttcccctgc ttgtttggat gaatgaatag 1440
aaggcatatt tataaagttt gcagaagaca actaaaacag ttgagagggc tatgttgata 1500
ctgacctgtg cttctcttgc ttttttattt gctgcttttc agtaaaatat gaaagaatca 1560
aatttctggt gattgctttg aagagttctg tggaagtcta tgcgtgggca ccaaagccat 1620
atcacaaatt tatggccttt aaggtaacaa catcaagtga atttaaaagt agtattggcc 1680
attcaagctg caaccaagag tcagggaatg tgtttaaaaa gtctgaatgt taaaattgct 1740
aatataaaag ctatgtgcta atatagcata taactttatc ataaaccatt tctaatgtaa 1800
taagcttagt taagctgctt tctaagccca cagtgagaag gagagagaga taaatgttgg 1860
gtagacactt taatcgatgt ggcaatgtgt tcacagagga aaagagaaca gtacttccac 1920
ccttcagtta aaaaggtgac cttcacctga gtcatggaag cgtgtaaaga tttagatgtg 1980
tttttgataa caaaactgtg tctatcgggc agttttaaga tatatctgtt cataaaatac 2040
taattaaaaa ttaaattaca gaaattctga tgacaacatt atatactaag tgaaaaaagt 2100
taaaatattt catatgattc catttttgtt tcaataaaaa actcagctat aacatctgaa 2160
ctaatgtaca aattaagatg tttttgccat tttgcatgta tacagtttta ggaaagtaaa 2220

tgatggagta cttagtctta aaattaggac tgttttcatt tgtgagttca caaaaatact 2280
catgaaattt acaaatatac ctcacattgc ctggtgattg gctttttaga atagtttttt 2340
tatattttat tgaaggggta ggtttcattt atttgcaaaa tttgtgtttt tggattgctt 2400
actgcttgat ttcccagtga agcaggatag atggagtcac aatattcgct taaaaaataa 2460
tattcactta aaaaataaat ccaagtgtta ctgaataaag agaattggtt atacagttat 2520
attatcttct gagatctggc cttaatatcc tttatatacc aggtaccgta ctagttggtt 2580
ttatacatat taccttattt aaagctgctg tttcattatc gtagtctcgt gaactgtggg 2640
tagtgatgtc agtgaaaaat ggagaccacc agcacaatcc aggctgttgt agcacataca 2700
gccttttcac cattttagtc tagtcagaaa attagagacc tttatagttc aaatagctac 2760
tagtatgatg atagtgatac aattttcagt gtgtgactcc tacaactcct ctcgctctac 2820
tgtgcatttg aatagttgag tagcattttt aggaaagtcc tcactatttt actttgcatg 2880
attttctgat caaggcagcc aaaagcacag taaatgacag agcagaaatc ttgatctgga 2940
aagggagatt tggaacatat cttctggaag aagtgtcttc tagatgctaa ttaacaggca 3000
aaaacgtaat aaagactaat tttgtagagt attgttgcct tacggttgtt gccagtgtgg 3060
ctcagtaatt gcataactga gtatgttggg tcttctctag tttgatctat tagaagtaag 3120
ttctccggcc gggcgtggtg gctcacgcct gtaattccag cactttggga ggtcgaggtc 3180
aggagatcaa gaccatcctg gctaacatgg tgaaaccccg tctctactaa aaatacaaaa 3240
aattagctga gtgtggtggc gggcacctgt agtcccagct actcgggagg ctgaggcagg 3300
agaatggtgc gaacctggga ggcggagctt gcagtgagcc gagatggcgc cactgcactc 3360
cagcctgggt gacagagcga gactccgtct caaaaaaaaa aaaaaaaaaa aaaaa 3415

<210> 30
<211> 55
<212> PRT
<213> Homo sapiens

<400> 30
Met Phe Met Lys Ile Tyr Thr Ser Ser Val Pro Leu Phe Arg Gly Met
1 5 10 15

Leu Ser Cys Leu Ala Leu Ser Cys Trp Cys Ser Leu Ser Ala Pro Leu
20 25 30

Ser Ser Trp Val Asn Gly Asp Cys Gly Ser Cys Leu Ser Ile Ser Asp
35 40 45

Ser Ser Asn Asp Thr Gly Lys
50 55

<210> 31
<211> 2967
<212> DNA
<213> Homo sapiens

<400> 31
gatgaagtgg agcagtgagt gtgagcctca acatagttcc agaactctcc atccggacta 60
gttattgagc atctgcctct catatcacca gtggccatct gaggtgtttc cctggctctg 120
aaggggtagg cacgatggcc aggtgcttca gcctggtgtt gcttctcact tccatctgga 180
ccacgaggct cctggtccaa ggctctttgc gtgcagaaga gctttccatc caggtgtcat 240
gcagaattat ggggatcacc cttgtgagca aaaaggcgaa ccagcagctg aatttcacag 300
aagctaagga ggcctgtagg ctgctgggac taagtttggc cggcaaggac caagttgaaa 360
cagccttgaa agctagcttt gaaacttgca gctatggctg ggttggagat ggattcgtgg 420
tcatctctag gattagccca aaccccaagt gtgggaaaaa tggggtgggt gtcctgattt 480
ggaaggttcc agtgagccga cagtttgcag cctattgtta caactcatct gatacttgga 540
ctaactcgtg cattccagaa attatcacca ccaaagatcc catattcaac actcaaactg 600
caacacaaac aacagaattt attgtcagtg acagtaccta ctcggtggca tccccttact 660
ctacaatacc tgcccctact actactcctc ctgctccagc ttccacttct attccacgga 720
gaaaaaaatt gatttgtgtc acagaagttt ttatggaaac tagcaccatg tctacagaaa 780
ctgaaccatt tgttgaaaat aaagcagcat tcaagaatga agctgctggg tttggaggta 840

aatggtttct gtgtctatgt tacgtgtgta tgtatgttca tgtataacag ataattcata 900
gaatcctgcc tgtctttaga tgaggcgctc aggacctgtc aaatactaat aaaagcttaa 960
cacaaactca actttcatga agtcatagaa tctgagagct gtaaagaacc ttagtgatta 1020
agctaaaaag tgtaagtata aaagaatttc actgttgaaa actcaagact tttaaaaata 1080
aatcactatc tgttcctatg cataagttct ttttaaaata tataccctaa aggcctatga 1140
ctttattcta gtcatctctt tctcaggcag gcttgttgac tagagtaggt ctcaaggcca 1200
tggaggagaa atgaactctg tcatattgca actgatagaa ttgagagtgt gagaagcaag 1260
gccaatgatt ctacaagcat gaagcaaaga agctggtgtg ggcccaatat cataaagggc 1320
tacagagaag gtttttctcc tgtactgtct actgtctcaa tcacctggat catgcaatga 1380
gcattacaca caatgtttaa gtgaaggacc aacaggcctt gtctctgttc cttgcaggtg 1440
tccccacggc tctgctagtg cttgctctcc tcttctttgg tgctgcagct ggtcttggat 1500
tttgctatgt caaaaggtat gtgaaggcct tcccttttac aaacaagaat cagcagaagg 1560
aaatgatcga aaccaaagta gtaaaggagg agaaggccaa tgatagcaac cctaatgagg 1620
aatcaaagaa aactgataaa aacccagaag agtccaagag tccaagcaaa actaccgtgc 1680
gatgcctgga agctgaagtt tagatgagac agaaatgagg agacacacct gaggctggtt 1740
tctttcatgc tccttaccct gccccagctg gggaaatcaa aagggccaaa gaaccaaaga 1800
agaaagtcca cccttggttc ctaactggaa tcagctcagg actgccattg gactatggag 1860
tgcaccaaag agaatgccct tctccttatt gtaaccctgt ctggatccta tcctcctacc 1920
tccaaagctt cccacggcct ttctagcctg gctatgtcct aataatatcc cactgggaga 1980
aaggagtttt gcaaagtgca aggacctaaa acatctcatc agtatccagt ggtaaaaagg 2040
cctcctggct gtctgaggct aggtgggttg aaagccaagg agtcactgag accaaggctt 2100
tctctactga ttccgcagct cagacccttt cttcagctct gaaagagaaa cacgtatccc 2160
acctgacatg tccttctgag cccggtaaga gcaaaagaat ggcagaaaag tttagcccct 2220
gaaagccatg gagattctca taacttgaga cctaatctct gtaaagctaa aataaagaaa 2280
tagaacaagg ctgaggatac gacagtacac tgtcagcagg gactgtaaac acagacaggg 2340
tcaaagtgtt ttctctgaac acattgagtt ggaatcactg tttagaacac acacacttac 2400
tttttctggt ctctaccact gctgatattt tctctaggaa atatactttt acaagtaaca 2460
aaaataaaaa ctcttataaa tttctatttt tatctgagtt acagaaatga ttactaagga 2520
agattactca gtaatttgtt taaaaagtaa taaaattcaa caaacatttg ctgaatagct 2580
actatatgtc aagtgctgtg caaggtatta cactctgtaa ttgaatatta ttcctcaaaa 2640
aattgcacat agtagaacgc tatctgggaa gctatttttt tcagttttga tatttctagc 2700
ttatctactt ccaaactaat ttttattttt gctgagacta atcttattca ttttctctaa 2760
tatggcaacc attataacct taatttatta ttaacatacc taagaagtac attgttacct 2820
ctatatacca aagcacattt taaaagtgcc attaacaaat gtatcactag ccctcctttt 2880
tccaacaaga agggactgag agatgcagaa atatttgtga caaaaaatta aagcatttag 2940
aaaaaaaaaa aaaaaaaaaa aaaaaaa 2967

<210> 32
<211> 250
<212> PRT
<213> Homo sapiens

<400> 32

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
1 5 10 15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
165 170 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Lys Trp Phe Leu Cys
225 230 235 240

Leu Cys Tyr Val Cys Met Tyr Val His Val
245 250

<210> 33
<211> 2926
<212> DNA
<213> Homo sapiens

<400> 33
tttagtcgga aatatgctag tagtaatcat tggaaaagct gatgaagcta caactgtggt 60
acgtgtgtgt gattttattt cttattggca tttctctgct ggcagttgga actgacagtg 120
atgggaatgt ggcaactgaa tgttttctct ctttcttggt tccttccatt tttatctcaa 180
cttttctagt gtgttgtccc cttttctaaa tggcattgac aaactcatca agatccagag 240
ataaacagtc catcgtttaa gaatatttta ttttgcatgt agaggaaaga attaaccaaa 300
gacgtttctg ctctgatact ttctaaagaa aacagactaa ttatatataa gtggtatcaa 360
taggtctgct tataagtatt gtcctatgta gagatttact ttttggtttt tacaagcata 420
gtttgcgctt ttagatgtct ctcaggtgaa aaatagaagt tggcagccct gagcaagcac 480
ctgtgacaca gggattttta ttttagtttt aaagtatgat atagagaatg aggtttttgg 540
tttgatttgg tttggttgtg ttttttagtt ctttattttt tatttggggg ttctcttagt 600
gatggcatat ttcaggtttc agtgacatag atcaagtaat tttaaaccga tttggttatt 660
ctatctaaga tgagggacat ggctattaag gtcaagccaa actatactaa aagtagtata 720
gggcagcagt taaaattatc ttttgaaaat caagtattac ctggtttctt ctgtcacaac 780
agaatagctg gttacctagt cagtcacagt tgcccttgcc ttcccttgtt agtccctgga 840
ggtacttgag tggaacagaa ggcagaatta gcaacagctc aatcacttta ggtagcattt 900
ctcctgaatt ctgctgccaa atcctcaggg tctatggatt ggttgaaata gtaaaatcac 960
acatagtgat ttcttgcaca gcgtagaggc gtttaatttt agtgtatagt gaacaaagaa 1020
ggaaaactgg gtcatataaa atttaacctt aaaacacaga ttataaatat ctttgaatgt 1080
taagccctag gcagacagac actctcattc ttaactctgg tatgcaagct ggccttgctg 1140
acagtggcat agttacatta actgtttttt aagttgcatg ttgtgatgtg aatgtttttt 1200
gtaaaagttg ccaagttaat cgagtcctaa ataagtagcc aaatggtaac tgagacccac 1260
tgtagacatt actcgcttta tattatttgc tttcaaatac taaaacctca gctgctaatt 1320

cagcgctcta ggtgtacagt gtctccttcc cttggctcct agcaatgtag ggaacttgag 1380
gttcttcagt atcttcagag attccttcca ggccacatat ttttatgcta atacttctat 1440
agttgcattc aatctacaag gagaaagtgt acattggtgc atgttttata aacccagaca 1500
cagatagcta aaaccataat tagtttttct atacccagag ctttgaatta aaaacagatg 1560
cttttttttt ccccaagagc agacagttct acattcctaa cattaggaat tggtgatacg 1620
agaagcagga tccagaattc agaatgattt agtgagactc ggtgaaaaaa atgcattttc 1680
ccctggctgt ttgaaaattt acttatttgc agataagtct agatttagtc ttggagatca 1740
aagtctttta tattttaaaa acttattctt tatattgatc aaacatggca tatgttagag 1800
aaccacttct tctgtcatgt ttatgtattt tggaattaag ttgtttgcat tcactttcaa 1860
aatctgccca tttctgttta tgtgcactta ccacagatgt gtcgggactt tgcctcaggg 1920
gagaggtact ttagcacctg tgtcactgag gagatggagt ggttgacaag tactgttgcg 1980
ctgtgtaact tggggtttgg ccctgtggac aatatattag cagaatgata ccacacaaaa 2040
gtattacagg attaaggcat gtaacttcta tggtagtcct tatgtatcag cgtataccca 2100
agttcagaaa ccacaggtgc atttttagac ctttacttag agaactaaag gcagttccaa 2160
ccatcagccc atatggcggg attaatgcat gaaaaccctc agagggtgtt gggacatcct 2220
acttccctgt cctcacccag tggaactctg gtgtgtgcct tgaggataag gaagtagagt 2280
ggaaactcat cctatcattg agtattctca atatttggc cttccctctg gaattatgag 2340
aaatttaaca aagtctcagg aacctttaga atccattgtc caacactgct agaaaaactg 2400
taggaggtac atggagaatt cctatagttc ttaggtaagt gcaagacatg gcacagggat 2460
ccctatccac ataaagggga atctggatgc tgcacacctc aattctgaga aatccctgac 2520
tgaacttgga attatgacag taaagttttc gtcctttagt tttctagagc agctcacaga 2580
aattttaaaa agtaaaacaa ggccaggcgc agtggctcat gcctgtaatc ccagctcttc 2640
gggaggctga ggcgggcaga tcacgaggtg aggagatcga gaccatcctg gctaacaggg 2700
tgaaaccccg tctctactga aaatacaaaa aattagctgg gcatggtggc gggcgcctgt 2760
agtcccagat gctcaggagg ctgaggcagg agaatcgctt gaacctggga ggcagaagat 2820
tacagtaagc caagatcgcc ccactgcact ccagcctggg cgacagagtg agactccgtc 2880
tcaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2926

<210> 34
<211> 55
<212> PRT
<213> Homo sapiens

<400> 34
Met Lys Leu Gln Leu Trp Tyr Val Cys Val Ile Leu Phe Leu Ile Gly
1 5 10 15

Ile Ser Leu Leu Ala Val Gly Thr Asp Ser Asp Gly Asn Val Ala Thr
20 25 30

Glu Cys Phe Leu Ser Phe Leu Val Pro Ser Ile Phe Ile Ser Thr Phe
35 40 45

Leu Val Cys Cys Pro Leu Phe
50 55

<210> 35
<211> 3283
<212> DNA
<213> Homo sapiens

<400> 35
aaaagctgaa tcagaaatga agttaattaa acacatgtac acctgccaca aatttgtctc 60
tgcactttta cttgctgttg ttcaattcac agtgtccaag agaaaaataa attatttctc 120
agaaaaagtt catccattct tagtacttag aacaatcaaa atacattatg atgaattgta 180
tttaatatat gtctattttg atactggatt taaagaacat ttaagggaag aatgttctct 240
tgatttgcta aactaacagt aggaaccaag tcaatgcgta ttgaatataa caaaattatt 300
cctttatgtt tccagaagca gcatcaaaaa taattgtatt tctaagtcac atacagcaaa 360
ccattatata tttgcatttc atatttttaa aagtactcta taggaaattt ttaatgtatc 420

```
ctacatacac atagctgtat gaaaatagtt tattcatgga ggaattttcc tgtagaatac 480
ttatatatct gccttacaat taaaaccaaa catgtattac tatttttgtt acagaagctt 540
tatatagaaa atacagttaa attcatccaa ataaaaaatt ttaatcttga gtctgggaaa 600
tgtatacaaa ggacttcatt gagccattct cttgactttt gaatatattt gaaaattttc 660
gtatgaattt tcagtaacca catgtattcc tttcagatca tactagaatg cagttcactt 720
tcctatttga taaactcatg ctcatttttt tgaatttgat acggtatttc caaaatatta 780
tctgattgga aataataaac atttgcttaa actgtaacga aggccaaagt gctgggatta 840
caggcatgag ccaccgcgcc aggcccaaaa ctaaaagtaa tttttatgtt caatacctta 900
ttgaaacatc ttgactctca taaataaaca ttgccaaatt ttaacatact gtctaaagtt 960
agcaatgaat aagcatatgt ttcttaatct gtggccggtg aaaaatttgt tatattgtgt 1020
cagtcaataa gattttagta gtaaatgtgg gtagattcat gaaacgatca aatttctgga 1080
caattaacat tgcacaaaat taatggcata aaacatattt acaaagaact aaacatcaaa 1140
tgtgaggtca tctgagcata tagtagacct tactctttct ttcactttct ataaaacatc 1200
tgcttaggga aaacctagac ttagaaataa taaaaatgca gagaccaaag actggatttt 1260
tttaaatgta actttcttag aaaaaagatt ctgcaaaatg tcagtgattg aatgtatttt 1320
taacgtttga gcacagcatg gcacaataaa acaaatgtca gccatctgac ttgggttgta 1380
ctttacaagt ttatgactat tgcaagagga caaaatactg aggttgctga aggtaaagtg 1440
ttttgttctg tgggccttta gcctttctcg ttttgatctt cctctttaat ccataggtgg 1500
tctgatgggt ggagacctca cgtctggtgc aggcaccagt gcaggtaagc ccagactcca 1560
tactgcagta tgtatcattg ttctgagttc ttctactagg tgatttgcag gacaaagtct 1620
tttgaacaaa taaagttaag agatctgtga gaggcatgga aaaatgacac caagaatttt 1680
taaagcactt ttctgaagca ggagtggtta aatagtaact tagaagaaaa ctatttatta 1740
actagaacct tcccttaataa agcttcaact ggtcagcaga gaattaaggg ctctgatcca 1800
atcaacttaa tcctggatac catccttgga cacaagagta cctttagcaa accatacttt 1860
ttgtgttctc tgttaatcat ttcacattaa atatgaatca ttttccagcc aaagaagtat 1920
tgaacttcta tgcatttcta aagaagagta cataaagaaa aggaggggtt aagattttaa 1980
ttattcaaca atactgttaa taaaataaaa tcacattggc attaaaatga gctcttagac 2040
aacatgaata taatgcatcc ccaaaagacc ctaaaatata tttcagctaa gaacttctta 2100
cactgtgacc aataattgtc tcagtcacat ttctccaggt ttccgtgtta atttgtaata 2160
ttgagattat tgagatatcg atgtcatttt caatgcagag gcaagatagc acaatacttt 2220
caaatgccaa ctgcagttca ctattggcat aacaagtaac catggtaatt tctgcagctg 2280
gaacatgcta tacatttaaa atagtaggag gcaggcatga atgacacaag gttatgtttg 2340
aaatgtcaaa aaaaatcaag tttattgaaa tagacatgga tagcctaatt aaaatatttt 2400
gccagggtca agtagaatag cctgctaatt ataagaaaga agataaagaa aattggttta 2460
caaatacatt tttataaata tatctatttg agggtagagt ttctctgttc tgatgctggc 2520
tcttcactaa ttcactgaat aatgaagaaa aagtattaga cctacacagt gattagcaaa 2580
caagatgaat aacactagct tcctatttta tatatctttt gaaaattagg tcgagccaaa 2640
ttagtgtgta aactcacgta gtattttgct ggacatggaa atgaaatttt ttccctcaaa 2700
aaatactttg tggtttgtag cctcaaaatg agagaaccag atcaaatcca gaccaatgtt 2760
tcttggatcc aagtctctac caaacactat gattagaaag aatggtgagg actgagaatt 2820
gggtggtcac aaagaccaag atataatata agaaaaatgg tttagatgtt atgatgtttt 2880
acccaatatc tcactgcacc gatttgcttg ccattatgga aacagctagt agtggttctg 2940
aaagtcatta aaagtagtaa aaaagggccg ggcgcggtgg ctcacgcctg taatcccagc 3000
actttgggag gccgaggcgg gcggatcacg aggtcaggag atcgagacca tcccggctaa 3060
aacggtgaaa ccccgtctct actaaaaata caaaaaaatt agccgggcgt agtggcgggc 3120
gcctgtagtc ccagctactt gggaggctga ggcaggagaa tggcgtgaac ccgggaggca 3180
gagcttgcag tgagccgaga tcccgccact gcactccagc ctgggcgaca gagcgagact 3240
ccgtctcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa                   3283
```

<210> 36
<211> 79
<212> PRT
<213> Homo sapiens

<400> 36

```
Met Lys Leu Ile Lys His Met Tyr Thr Cys His Lys Phe Val Ser Ala
  1               5                  10                  15

Leu Leu Leu Ala Val Val Gln Phe Thr Val Ser Lys Arg Lys Ile Asn
             20                  25                  30
```

Tyr Phe Ser Glu Lys Val His Pro Phe Leu Val Leu Arg Thr Ile Lys
35 40 45

Ile His Tyr Asp Glu Leu Tyr Leu Ile Tyr Val Tyr Phe Asp Thr Gly
50 55 60

Phe Lys Glu His Leu Arg Glu Glu Cys Ser Leu Asp Leu Leu Asn
65 70 75

<210> 37
<211> 2248
<212> DNA
<213> Homo sapiens

<400> 37
tgatgttcct cgcctgtctc tgcctggaaa actggtcttc ccaagctcca ctggcagcca 60
cttctccatg ttgggcatcg gagacatcgt tatgcctggt ctcctactat gctttgtcct 120
tcgctatgac aactacaaaa agcaagccag tggggactcc tgtggggccc ctggacctgc 180
caacatctcc gggcgcatgc agaaggtctc ctactttcac tgcaccctca tcggatactt 240
tgtaggcctg ctcactgcta ctgtggcgtc tcgcattcac cgggccgccc agcccgccct 300
tctctatttg gtgccattta ctttattgcc actcctcacg atggcctatt taaagggcga 360
cctccggcgg atgtggtctg agcctttcca ctccaagtcc agcagctccc gattcctgga 420
agtatgatgg atcacgtgga aagtgaccag atggccgtca tagtcctttt ctctcaactc 480
atggtttgtt tcctcttaga gctggcctgg tactcagaaa tgtacctgtg tttaaggaac 540
tgccgtgtga ctggatttgg catttaaagg gagctcgttt gcaggagaga ggtgctggag 600
ccctgtttgg ttccttctct tcctgcggat gtagaggtgg ggcccccttcc aagagggaca 660
ggcctctccc cagcgcgcct tcctcccacg tttttatgga tctgcaccag actgttacct 720
tctgggggag atggagattt gactgtttaa aaactgaaaa cagcgaggag tctttctaga 780
acttttgaac actaaaagga tgaaaaaaat tagcaaaccg aagtttcttc aatgacccct 840
cgagaacttt gggaccagtt tcctataggg gactcagttt cagagaactg agacagaagc 900
tcttctgtcg ttatattctt ctttcctttt tttggattta ttaaatattt tctgtggtgt 960
gaagtgactt attaaatcca cagacattga gtgacttctt acaacatcca cataagaatt 1020
tgttgtaatg agttcatgtc cacccagatg ttgtgttggc agtgaacaag ggcacggttt 1080
ttatacatac gtacatatat atatataaac acacacatag atatatatga ataaacaaaa 1140
atgaaatcct gctaagatca cgctgtgtag ctgacagggg cttgctgtcg ttttgagcat 1200
gtcgagcagt ttactgtggc ttccttgtat atggataagc tgctgtcctt ccccttcaca 1260
actgaccccg cagttacaaa ctagtatagc atttgtgctg attgatgata gactcatgga 1320
cttcaggagc ccttacttgg ttttgatcag tgtagcaaat tagggatgaa gagttcaaac 1380
cttttggccc tttctttctt ttctaggctt ctccctcgca gggtgttccg tagtttcttc 1440
tcgagccaat gcatgtatta tagcagcagg tgtctttgtg ctttctcatc atagtaacgt 1500
actacttgta aatacatttt tctattttct attttttgt atttttttt ttgacatttt 1560
gtttcattgg tgtgctgtat attttccatg ccctcactcc tttaagaaaa aaaaaaagga 1620
aaaaagcaac acaatcctgt ccttgctgtt gtgattatag tcttggttta cctgtggtga 1680
caaccgggtg ttggggacac atgtcaaatg cccctctgag atgggcccta aattccagta 1740
actggggaaa gaaccagctg ctgtgtcctg agagcctggc cctgtgctgt ggtctctgct 1800
gcaagcccag atttctggga gtaactagtg ttaggtctgc tgacctttac ctaagcagcc 1860
cctgcctggt aagaaggtgc ccattgttca gaggcaaaga gaagcctgcg gttggcatga 1920
ggatgcctga caacaaaggc tggagaaggg ccctgagttc cagcctctcc ccaagggtcc 1980
ccgccccagt ggctgcctct gtcttgacct gtgtaatgaa ttagtgtgct gtgtcactgt 2040
ggcttgaagt cactgtggat cgagctcaca gggggcaccc atcctgttgt caacagagtc 2100
tgaagcagtc agggtgttgg attcctctgt tgttgtcatc aattcctgct gaggggtttc 2160
tggggttttg tttttaataa atgactcctt tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa 2220
aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2248

<210> 38
<211> 119
<212> PRT
<213> Homo sapiens

<400> 38
Met Leu Gly Ile Gly Asp Ile Val Met Pro Gly Leu Leu Leu Cys Phe
1 5 10 15

Val Leu Arg Tyr Asp Asn Tyr Lys Lys Gln Ala Ser Gly Asp Ser Cys
20 25 30

Gly Ala Pro Gly Pro Ala Asn Ile Ser Gly Arg Met Gln Lys Val Ser
35 40 45

Tyr Phe His Cys Thr Leu Ile Gly Tyr Phe Val Gly Leu Leu Thr Ala
50 55 60

Thr Val Ala Ser Arg Ile His Arg Ala Ala Gln Pro Ala Leu Leu Tyr
65 70 75 80

Leu Val Pro Phe Thr Leu Leu Pro Leu Leu Thr Met Ala Tyr Leu Lys
85 90 95

Gly Asp Leu Arg Arg Met Trp Ser Glu Pro Phe His Ser Lys Ser Ser
100 105 110

Ser Ser Arg Phe Leu Glu Val
115

<210> 39
<211> 931
<212> DNA
<213> Homo sapiens

<400> 39
tggggccgct tgggctgttg gtctccagag cagggccact gggcactctg tgatggggga 60
gcctttgtct gaaagcacag ccccctcgcc cttcctctcc ccatggcttc cccttcattg 120
gcattaatct gggcaccagc tctctccata gcagtgactt ccctcaccac tctcatctct 180
cagccttgcc ttttcttcct gacactgtcg ccccctcctc tcaggagaca ctgccgaggg 240
ccacctggca gaaggctgag ttaggcagca gggccgggag cgtctgccct ccacagggtg 300
ggggacagat aggctaagcg actcccagct tgctaccctc agtggccagt gtgggcgtgg 360
gcggtttggg gcgcttggct ggtggtggcc actgcatccc ttaatttatt tctctgctgt 420
ttctgttctt gagaaattgg gggtgggagt cctacacaga ggctgcccct accctcacct 480
gagttgtaca tttttttgtg atgggtttta ttttttatta ttttatttta ttttttttt 540
tttttgattt atgatgactc cacccctctt catcaccccc gctcccaggc caggctcagc 600
gattaagccg agcccttgcg tcctaggaag gggccttgcc aacctcagcc ctcctgcccc 660
acactcctac tgcggctcag accaagggct ccccctccct cccttccccc ctcctgccct 720
atggaacagc ccgggtgctc tgaggggct gggagggcat ggcttggctc ccaaaggggg 780
taggggcccg gggcacccag gcaaggtggc ccctccccgt ctagcccct cctccccaac 840
cctgcactta gtttctcctc tggatcaaac acgtaataaa gagaatgttt ggaatctgaa 900
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 931

<210> 40
<211> 53
<212> PRT
<213> Homo sapiens

<400> 40
Met Ala Ser Pro Ser Leu Ala Leu Ile Trp Ala Pro Ala Leu Ser Ile
1 5 10 15

Ala Val Thr Ser Leu Thr Thr Leu Ile Ser Gln Pro Cys Leu Phe Phe

20 25 30

Leu Thr Leu Ser Pro Pro Pro Leu Arg Arg His Cys Arg Gly Pro Pro
35 40 45

Gly Arg Arg Leu Ser
50

<210> 41
<211> 3625
<212> DNA
<213> Homo sapiens

<400> 41
tggctaggct ggtcttgaat tcctgacctt gtgatccacc cacctcggcc tcccaaagtg 60
ctgggattgc aggcatgagc caccacgccc ggccgttgga acatattttt atttaattta 120
attaatttat ttatttattt ttgagatgga gtcttgctct gtcgcccagg caggagtgca 180
gtggcgcgat ctcggctcac tgcaagctcc acctcctggg ttcacaccat tctcctgcct 240
cggcctccca agtagctggg actactcgcc accactccag ctaatttttt tgtattttta 300
gtagagacgg ggttttacca tgttggccaa gctggtctcg atctcttgac cttgtgatcc 360
acccgcctca gcctcccaaa gtgctgggat tacaggaatg agccaccgct cccggctgct 420
ggaattttta ataagcacgt gagctggtgt gatgagaacc ccatgtagga gtttttaccg 480
atttcttctt cggcagcctt gttgagtgcc tactgtgcgg caggctttgc tgattcagca 540
gtgagtccac caagcaagcc ctgcccgcag gatgagtcca gcaggggagg tggcagcgag 600
gcagccttca ggccacagcg gctggcctct gtccttggtg ctgaggctgc gctggtggga 660
aaaatcatcc agcatcaaaa accccccacc gtcaaaaagc ttgtgtctta gcaagtggga 720
gacagctgag tgggccctcc ctcagttagt gattcctaac ctagtccttc gacctttctc 780
tttgtttgat accaagttta tttttttaaa tttttttatt atctatttat ttatttctgg 840
gacggagtca cgctctgtgg cccagactgg atttcagtgg tgtgatctcg gctcactgcg 900
gcctctgcct cctgggctca agcgattctc ctgccttggc ctcccgagta gctgggatta 960
taggcgtgca ctaccatgcc cagctaattt ttgtattttt ggtagagaca gggtttcacc 1020
atgttggcca ggatggtctt gatctgctga cctcgtgatc cacccacctc ggcctcccga 1080
agagctggga ttatgggaat gagccaccgc acctggccct cggcctcccg aagagctggg 1140
attacgggaa tgagcgaccg cgcccggccc cagattttcc tttggttgcc atctttgtat 1200
acttcttaac tctccgtttg atcaaaagat agttttggct gggcatggtg gcccacgcct 1260
gtggtcccgg tacttcggga ggccgaggtg ggaagatggc ttgaggccag gagttccata 1320
ccagcctggg ctgcagagca agaccctgtc tttacaaaaa ataagaaaac ttagctgagt 1380
gtggtgaccc acgcctgtgg ctgcggctac tcgggaggct caggcaaaag gatcccagga 1440
gtttgaggct gcagtgagcc gtgatcgctc cactgcactc cagcttgggt gacaggcatg 1500
cgtggagtgg cagtgctaac ggctggtgtc tcgcactgtt ggcctgtgaa ggtacgtgaa 1560
gctgaaagcc tggaatggct ggaaaggggt catcaggcag gcggcccctg ctgctggggc 1620
tgctggtggc cgtagccact gtccacctgg tcatctgtcc ctacaccaaa gtggaggaga 1680
gcttcaacct gcaggccaca catgacctgc tctaccactg gcaagacctg gagcagtacg 1740
accatcttga gttccccgga gtcgtcccca ggacgttcct cgggccagtg gtgatcgcag 1800
tgttctccag ccccgcggtt tacgtgcttt cgctgttaga aatgtccaag ttttactctc 1860
agctaatagt tagaggagtg cttggactcg gcgtgatttt tggactctgg acgttacaaa 1920
aggaagtgag acggcacttc ggggccatgg tggccaccat gttctgctgg gtgacggcca 1980
tgcagttcca cctgatgttc tactgcacgc ggacactgcc caatgtgctg gccctgcctg 2040
tagtcctgct ggccctcgcg gcctggctgc ggcacgagtg ggcccgcttc atctggctgt 2100
cagccttcgc catcatcgtg ttcagggtgg agctgtgcct gttcctgggc ctcctgctgc 2160
tgctggcctt gggcaaccga aaggtttctg tagtcagagc ccttcgccac gccgtcccgg 2220
cagggatcct ctgtttagga ctgacggttg ctgtggactc ttatttttgg cggcagctca 2280
cttggccgga aggaaaggtg ctttggtaca acactgtcct gaacaaaagc tccaactggg 2340
ggacctcccc gctgctgtgg tacttctact cagccctgcc ccgcggcctg ggctgcagcc 2400
tgctcttcat cccccctgggc ttggtagaca gaaggacgca cgcgccgacg gtgctggcac 2460
tgggcttcat ggcactctac tccctcctgc cacacaagga gctacgcttc atcatctatg 2520
ccttccccat gctcaacatc acggctgcca gaggctgctc ctacctgctg aataactata 2580
aaaagtcttg gctgtacaaa gcggggtctc tgcttgtgat cggacacctc gtggtgaatg 2640
ccgcctactc agccacggcc ctgtatgtgt cccatttcaa ctacccaggt ggcgtcgcaa 2700

tgcagaggct gcaccagctg gtgccccccc agacagacgt ccttctgcac attgacgtgg 2760
cagccgccca gacaggtgtg tctcggtttc tccaagtcaa cagcgcctgg aggtacgaca 2820
agagggagga tgtgcagccg gggacaggca tgctggcata cacacacatc ctcatggagg 2880
cggcccctgg gctcctggcc ctctacaggg acacacaccg ggtcctggcc agcgtcgtgg 2940
ggaccacagg tgtgagtctg aacctgaccc aactgccccc cttcaacgtc cacctgcaga 3000
caaagctggt gcttctggag aggctccccc ggccgtcctg agggggacca ggcagccctc 3060
agcagccaca ggccttccag gagctgttat cactaccagt ttctggcaca attccagcac 3120
aattatgaca attcagagaa gcaagtcaaa ggactgggca cctgcctctg acagacacca 3180
gaccaggtct tgttggcacc ccgggagcca ctgcccaggg tgatggtggc cagctcaggg 3240
cttcctgcgg gtgactgtcg cccagaccag gtgccattca tgactaatca ggagcagcgg 3300
gctcacccag gcacctgtct gccaggaggc cacgtgtgtc ctgcccaccc agggggagct 3360
gtattttggc agcaccccac gcttgctgcc cgagggcctc ttggggcacc taagacagca 3420
ccccctctca ggggagacca tggtggcccc ggccgcaccc ccccaccctg gtgccaccac 3480
tgcaactttt gtattcacag gcatcccatc tccatcacag ataaaatctt aggagataaa 3540
cacattcaaa aaggaatgag ataaaaagaa taaggcaata aatgttgatt ggaacctctc 3600
aaaaaaaaaa aaaaaaaaaa aaaaa 3625

<210> 42
<211> 488
<212> PRT
<213> Homo sapiens

<400> 42
Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu
1 5 10 15

Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys
20 25 30

Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His
35 40 45

Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val
50 55 60

Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro
65 70 75 80

Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln
85 90 95

Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp
100 105 110

Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr
115 120 125

Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys
130 135 140

Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala
145 150 155 160

Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser
165 170 175

Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly
180 185 190

Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg

```
        195                 200                 205

Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr
    210                 215                 220

Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly
225                 230                 235                 240

Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly
                245                 250                 255

Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu
            260                 265                 270

Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr
        275                 280                 285

His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu
    290                 295                 300

Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu
305                 310                 315                 320

Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys
                325                 330                 335

Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu
            340                 345                 350

Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe
        355                 360                 365

Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro
    370                 375                 380

Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr
385                 390                 395                 400

Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys
                405                 410                 415

Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile
            420                 425                 430

Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His
        435                 440                 445

Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu
    450                 455                 460

Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu
465                 470                 475                 480

Leu Glu Arg Leu Pro Arg Pro Ser
                485


<210> 43
<211> 2861
<212> DNA
```

<213> Homo sapiens

<400> 43
tttgtttggg gaagtaaaat ccttaaggga ctaaattaat gcttgggtgc attaaaaaga 60
acaaaacatt cccacatgtt ggggtcattg ggagatgccc ggttttgcgg gttttatttg 120
tttaatttta ttctgtgttt tctcttggct ctttgggtct ttcccgggta cactagatgg 180
ctccatccca aggcatcttg tcataaaaca gctttccccc accccatatc atgggaaaag 240
ggggagaaat atagccccta gcctaataac ttatcatttg taaaatgact tataaaaata 300
ttacctcaat ggtaggagac atccagactt gtatatttca gtggaaatac aaaaccactt 360
cagagaccag ggtatctcct ctggaaggat ctaagagaag gtaagacaga ttaggacatc 420
gaaaaggagg atggagccag gtgccatggc ttgagcctat aatccgaggc tgaggtggga 480
ggatcacttg agcccaggag tttgaggttg cagtgagctg tgatcacacc actgcactcc 540
agcctgggtg acagagtgag actctgtctc aattaatttt tttttttaa aggaggagga 600
tctccatggg taagtggttt ctacccgcat gggtagagtt ctgcctctgg tccttctcag 660
ggggcacttt caccaagagc agtgtaatta tctctgaaag agcaagtcag cttgtgccgc 720
atccccaacc aatccacagc ctggagtacc tttcaaggtc aaagtgcatg gccagctcca 780
ttgagacatt ccatttcaaa gcaccgtgct gacagatatc aaagtactct agcagggaaa 840
ataatttgtt tgctgtgtaa ggaagaatgt agacaagaca gataaatctg aaggtcatgt 900
ggcatcaggg aaagggcatg gctgtgtctt ttgcacccaa tatgaaacat cttctcccaa 960
cactgcttta atggaagttc taggaaccaa tttagctcag gcatttgact cctacagcag 1020
aagttctgag cctgaccaca gatggtgtgt aatctatcaa acacacccct ggccaagttg 1080
ggtcctatag gacctggtac tatgtactat tgtaacttct agttccctaa gaggtacctg 1140
ttttcagtaa aaaggggtcc tgagttctgt gcaggtggaa gagctacccg agaactacct 1200
gagttctgtg caggtagagt cccatttctt atgggacctg tgtgctcctg agaactctta 1260
cttgagacat caaaaagaag cagcaagagc ttctgggaca gagactgctt ggccagcttt 1320
gtaagtaagt ggctgcctcc aatgtgatgt gagtacatgt tgggcagtct cactgtccta 1380
aggtatgtct tctttccacc tcccactgcc cctcccctgc cacctatcaa tgatgccttg 1440
gttcagtcat tagaaatctg ttgctttgag ttctgaaata ttttcacctt aaaaaaaatg 1500
ctgaaaatac acattctcct gggaagacga taaacagcta gctaagaagc cgaggttcag 1560
tggtggcagc aggaaggaca ctgccacaaa ttttgtctat ttcatatttg tcccctagag 1620
ccagccctag caaatgtgtg agttgggagt agttaatagt aaataagact ctgactttac 1680
acaagctaca cattttatac ttttcataaa ccacaaagtc tctctagaat tttttctgcc 1740
ttcactaaaa ttggactgta gccaagatat aaagcaagtc atttggaacc tgccgagtga 1800
gcactgaagc tactttatca tgagatgtgt gttaagaagg ctgcagccca caggagtcca 1860
gggaaggcgg ggaccacaga ggcacagagt ccagcacttg gccgctcatg ggccttcttt 1920
ctgcctcaga ggacgggggc agagaagtga tgaagggaaa tgttcttaga ggaggaaata 1980
tcctttgtcc tgttcagaga gaccagggcc ctaccattag gcatactttc agaagcaacc 2040
tggagaacag ctatcaatca tattcaaaac cagtacaaga actgctgcct ggtaccctgt 2100
gagtcatttc tatgaaattc catataaaga atgatgataa gtttacacac tgtgcaatct 2160
cacaatctga aaataaagtt gagttggctg tgttttctct gctcttgtca gaacattggg 2220
acaattggtc gttcaaaaac attcatcctc ttactgcaag tttatctggg tacttttacc 2280
tgtgtgttca aaggcatttc ttttcagcag tgatcattat aacttcacaa aaaaagatgc 2340
tgacggattt acttacaggg ccttaatgtt attttgtccc agccaacacc ctctaggtcc 2400
taaaagtcaa ggtacttcag tttatttggc aaacatgaca acattttttt tggccctggg 2460
cccaacagtt tgtacttcat gaaacatatt gtacatttta catagtttaa tttaaaaaat 2520
accttttaag ctagttgatc tttgactgtc ttatttatta taacctttca gcacattcca 2580
aggttttagt tactcaggaa ggagttaatt aaaatgattt tattttggtc tgatggatgt 2640
tttttaaaag gaaaattatt attatgaacc ttcagcctac tttcttgagt gccgtaaaag 2700
tgcttgtaaa tctttttttt tttttaagaa gaaagaaaaa aatggtgttt gacgttgatg 2760
gaaattcaaa aatatatatg gaactgaaac attaacttag ctaaaataaa agcaatctgt 2820
gtttgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2861

<210> 44
<211> 84
<212> PRT
<213> Homo sapiens

<400> 44
Met Lys Phe His Ile Lys Asn Asp Asp Lys Phe Thr His Cys Ala Ile
1 5 10 15

Ser Gln Ser Glu Asn Lys Val Glu Leu Ala Val Phe Ser Leu Leu Leu
20 25 30

Ser Glu His Trp Asp Asn Trp Ser Phe Lys Asn Ile His Pro Leu Thr
35 40 45

Ala Ser Leu Ser Gly Tyr Phe Tyr Leu Cys Val Gln Arg His Phe Phe
50 55 60

Ser Ala Val Ile Ile Ile Thr Ser Gln Lys Lys Met Leu Thr Asp Leu
65 70 75 80

Leu Thr Gly Pro

<210> 45
<211> 1556
<212> DNA
<213> Homo sapiens

<400> 45
acttgtcctg cctgctgctg gggtccctgg gctctatgtg catcctcttc actatctact 60
ggatgcagta ctggcgtggt ggctttgcct ggaatggcag catctacatg ttcaactggc 120
acccagtgct tatggttgct ggcatggtgg tattctatgg aggtgcgtca ctggtgtacc 180
gcctgcccca gtcgtgggtg gggcccaaac tgccctggaa actcctccat gcagcgctgc 240
acctgatggc cttcgtcctc actgttgtgg ggctggttgc tgtctttacg tttcacaacc 300
atggaaggac tgccaacctc tactcccttc acagctggct gggcatcacc actgtcttcc 360
tcttcgcctg ccagtggttc ctgggctttg ctgtcttcct cctgccctgg gcgtccatgt 420
ggctgcgcag cctcctaaaa cctatccacg tctttttgg agccgccatc ctctctctgt 480
ccatcgcatc cgtcatttcg ggcattaatg agaagctttt cttcagtttg aaaaacacca 540
ccaggccata ccacagcctg cccagtgagg cggtctttgc caacagcacc gggatgctgg 600
tggtggcctt tgggctgctg gtgctctaca tccttctggc ttcatcttgg aagcgcccag 660
agccggggat cctgaccgac agacagcccc tgctgcatga tggggagtga agcagcagga 720
aggggctccc aagagctcct ggtggtgcag cctgtgctcc cctcagaagc tctgctcttc 780
ccagggctcc cggctggttt cagcaggcga ctttcttcca atgctgggcc cagacttctt 840
gcctgggtgc tggcctgccc tctccggccg cttgctgcct gtctgctttc cttggtggct 900
ttgcctgggt gctgggcctg ccctctccgg ccgcttgctg cctgtctgct ttccttggtg 960
gctttgcctg ggtgctgggc ctgccttctc tggctgcttg ctgcctgtct actgccacct 1020
tcagaggggt tccttgctga gacccacatt gcttcacctg gccccaccat ggctgcttgc 1080
ctggcccaac ctagcgttct gtgccatgct agagcttgag ctgttgctct tcttcagggg 1140
aggaaatagg gtggagagcg ggaagggtct tgctcctaag tgttgctgct gtggcttttt 1200
tgccttctcc aaagacgcac tgccaggtcc caagcttcag actgctgtgc ttagtaagca 1260
agtgagaagc ctggggtttg gagcccacct actctctggc agcatcagca tcctactcct 1320
ggcaacatca ggccaacgtc caccccagcc tcacattgcc agatgttggc agaagggcta 1380
atattgaccg tcttgactgg ctggagcctt caaagccact gggatgtcct ccaggcacct 1440
gggtcccatg accagctccc cgtctccata ggggtaggca tttcactggt ttatgaagct 1500
cgagtttcat taaatatgtt aagaatcaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1556

<210> 46
<211> 224
<212> PRT
<213> Homo sapiens

<400> 46
Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg Gly Gly
1 5 10 15

Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro Val Leu

```
            20                  25                  30

Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu Val Tyr
        35                  40                  45

Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys Leu Leu
    50                  55                  60

His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val Gly Leu
65                  70                  75                      80

Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn Leu Tyr
                85                  90                  95

Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe Ala Cys
            100                 105                 110

Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala Ser Met
        115                 120                 125

Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly Ala Ala
    130                 135                 140

Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn Glu Lys
145                 150                 155                 160

Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser Leu Pro
                165                 170                 175

Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val Ala Phe
            180                 185                 190

Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys Arg Pro
        195                 200                 205

Glu Pro Gly Ile Leu Thr Asp Arg Gln Pro Leu Leu His Asp Gly Glu
    210                 215                 220
```

<210> 47
<211> 2446
<212> DNA
<213> Homo sapiens

<400> 47
```
atgtttctgt ccttgctgtt gactcctggt tcgcccagga gatcctggtt cacccaggga 60
tcacccaggg tggatgacag agggaatatt tactctgggt tcactgctgg agctccagtg 120
ccctgggagg ggagaggaga agcctgacct tgagcacagc tccagcctcc actccccact 180
cctatcgcag gctctgggct gtggtttcat tttccccagt tctctaacta ctcaggaagc 240
ccagagtttc tccctaaaga aaggtggccc tgcactcttt cctctcctcc aaaattaggc 300
ttcagtaatt gtcctctaag ttgatattta gaacttaaaa tctagacttc ttggatcacc 360
aagaaatatg caggaagttc cacgtgatct catgtgtgat agcacgtaac ttagtgctac 420
aggtgacagt tttatttttg gaggagtctt attttacata gggaaataga aaactaaatg 480
gcctcccttg aggcagccca agggctccac tggacccaga actctgagtt ctgatgctgc 540
ctatcatttg ctttttctca tgagctcctg gaccacctca tatcaccagc accctctacc 600
caaggtcctg gagccaacac tggagtaaaa gagcacaaga gaactcctta gaggtggaag 660
aagaacacag gtgtttgtgt cagacagcca gggtccaatc ctgcttctgc tgtagtgcaa 720
ttggctggaa gttgcagagg tttcagaagc tcatccaaga ttctggagcc cccgtctcca 780
gccctaatgc tgtccgcctt ttcacccagc caccacctgt ttcaggagaa cacacagaag 840
tgatgacctt ttctggacag gataccctct gaggtcaaat cattgggctt gtggccatga 900
```

gaccacagac tttgcctggc ttccagtgac tgtccgagat gacctgtgga gtgcaccgcc 960
tgtacttgga catcactgtc ttttccgatc catacccgtc atccttggaa tttcccctgt 1020
atccaaacct gttcctgata cagataaccc taaggaatat cttggatgtc ttcacggggc 1080
ttatgactta ttctgaggtt tacaaaatag aggcccccag ctgagcaaag agagggctgc 1140
agcgccgagg gaacagctgc tggactcacc ggagaggcct cctggagcac gccgggaccc 1200
cctccacccc ctggctttgg ctgcatccat ggctagtttg cctgaactat atctgagcca 1260
ctgagagtat ttattaagca gagaataatt ttgagtttca cttttataac ttttgtttca 1320
aaagttgttt tggataattt aatgaaatga ctgtaaacca gaattcccct tttcattatt 1380
tctttgtgtc gatataaaaa gagttgatga ttttaaaagc cagtgagatg tccctgtctg 1440
tggatgtcag cgggagcgtg ggtctgaag cctttctctg gtggctgtcc aggaagattg 1500
ccccagcttg cactcccttt tggcgggttc cagagccttc catttgaaag gagcatctct 1560
ccccactctg ccccacccag caccagctct tctggaaccc actgacttcc taaacacttt 1620
cttcctcctt cacctcattg aattcaagac tttagaaaac agccaaaaac tctagaggtg 1680
ggggtgggtg tgatctggaa atccctgctg taatcttttt aagggaatcc actggaaatt 1740
attaatttat gttttaaata aaaccattcc ttacttcaca gaatattaag ccactcactt 1800
tttaacagaa ctttgagata taattaaaat gccgtaaatt tcaccccccac acagtgtaca 1860
gttccaaggt ttccaatata gtcacagaag tctctgcaac aattaccaca atttagaca 1920
tgaagaccat ttgttggcag ccctacctgt atctatgtgt atatatataa ttttaatatt 1980
ggattagatg ttatagtatt taatattgta ctgttaccta tttgtgtctt tatattgctg 2040
tttttattc aggtgaataa taattatctc catatagtca tacatttata tagggttaaa 2100
acataccttt ttacaattca ataaattaaa ttggccaggc gtggtggctc atgcctgtaa 2160
tcccagcact ttgggaggcc gaggggggggg tggatcacct gaggttgggg gttcgagacc 2220
agcctgacca acatggagaa accctgtctg tactaaaaat acaaaaaatt agccgggtgt 2280
ggtggctcat gcctgtaatc ccagctactt gggaggctga ggcaggagaa tcactagaac 2340
ccaggaggcg gacgttgcgg taagccggga tcgcaccatt gcactccagc ctgggcaaca 2400
agaccaaaac tccatctcaa gaaaaaaaaa aaaaaaaaaa aaaaaa 2446

<210> 48
<211> 74
<212> PRT
<213> Homo sapiens

<400> 48
Met Thr Glu Gly Ile Phe Thr Leu Gly Ser Leu Leu Glu Leu Gln Cys
1 5 10 15

Pro Gly Arg Gly Glu Glu Lys Pro Asp Leu Glu His Ser Ser Ser Leu
20 25 30

His Ser Pro Leu Leu Ser Gln Ala Leu Gly Cys Gly Phe Ile Phe Pro
35 40 45

Ser Ser Leu Thr Thr Gln Glu Ala Gln Ser Phe Ser Leu Lys Lys Gly
50 55 60

Gly Pro Ala Leu Phe Pro Leu Leu Gln Asn
65 70

<210> 49
<211> 1231
<212> DNA
<213> Homo sapiens

<400> 49
ttgcggacac cccgtaccac ctgtatccgg cctatggctg ggtgatgttc gtcgctgtct 60
tcctctggct ggtgacaatc gtcctcttca acctctacct gtttcagctg cacatgaagt 120
tgtacatggt tccctggcca ctggtgttaa tgatctttaa catcagcgcc accgttctct 180
acatcaccgc cttcatcgcc tgctctgcgg cagttgacct gacatccctg aggggcaccc 240
ggccttataa ccagcgcgcg gctgcctcgt tctttgcgtg tttggtgatg atcgcctatg 300

gagtgagtgc cttcttcagc taccaggcct ggcgaggagt aggcagcaat gcggccacca 360
gtcagatggc tggcggctat gcctaaacca cctgtgccac ggccccctct ggggctgaag 420
ccgccgctgg gtcacagagc agggtcaccc tgcaagcctg aagctgggga gccctgcgtg 480
gagtcagccc aacagggact gcatttgctc ctctctgccc gtcagacata agctctcaca 540
gcgctaagga agcaggccca ggctggcagg catctcggct tgcaggaggc caactgctga 600
gacctcttct ccatccccct tattcagtgg aagatgacgg gggatctgag gctgtgtctc 660
tgccttgtct ttagaggact tcagcgtcca agactggggc ccacccttct caccagcact 720
aaatgcacta acaggactcc agacctgcag ccccagaccc gccgtagtat aagcctaaca 780
agcaacacgt agcaccttag tctttgttcc aggagagctg agcaagctgg tgaaaccact 840
ctccttcctt taaacaccgt ttcaaccaac ctctccctgg agccaacctg taaaaagtgg 900
gttgattgct gacagcatgg tcttccctcc ctgcatttca gacataccag ttactgaaag 960
caaatcagtt ttaagtgatt tctcagtgct gaaaagcctg tccaggtttc cttccctttc 1020
ccaagcctct ctctgtaata ctccctttgg gcgaagctaa catcggtgcc tccccgacct 1080
tgctgactag gcacatggga cgcaaaggag ggagggaagc aaggccttgc ctggcgagtt 1140
gtcatgtggt tggtggtgac tgttttattt tttttaataa aaataaagat gagagaaatt 1200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1231

<210> 50
<211> 113
<212> PRT
<213> Homo sapiens

<400> 50
Met Phe Val Ala Val Phe Leu Trp Leu Val Thr Ile Val Leu Phe Asn
1 5 10 15

Leu Tyr Leu Phe Gln Leu His Met Lys Leu Tyr Met Val Pro Trp Pro
20 25 30

Leu Val Leu Met Ile Phe Asn Ile Ser Ala Thr Val Leu Tyr Ile Thr
35 40 45

Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu Thr Ser Leu Arg Gly
50 55 60

Thr Arg Pro Tyr Asn Gln Arg Ala Ala Ala Ser Phe Phe Ala Cys Leu
65 70 75 80

Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe Ser Tyr Gln Ala Trp
85 90 95

Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln Met Ala Gly Gly Tyr
100 105 110

Ala

<210> 51
<211> 3290
<212> DNA
<213> Homo sapiens

<400> 51
tctctgtcaa ctgcttggac cagcatgttc ggaagtcccc cgagagcgtt gctttgatct 60
gggagcgcga tgagcctgga acggaagtga ggatcaccta cagggaacta ctggagacca 120
cgtgccgcct ggccaacacg ctgaagaggc atggagtcca ccgtggggac cgtgttgcca 180
tctacatgcc cgtgtcccca ttggctgtgg cagcaatgct ggcctgtgcc aggatcggag 240
ctgtccacac agtcatcttt gctggcttca gtgcagagtc cttggctggg aggatcaatg 300
atgccaagtg caaggtggtt atcaccttca accaaggact ccggggtggg cgcgtggtgg 360

```
agctgaagaa aatagtggat gaggctgtga agcactgccc caccgtgcag catgtcctgg 420
tggctcacag gacagacaac aaggtccaca tgggggatct ggacgtcccg ctggagcagg 480
aaatggccaa ggaggaccct gtttgcgccc cagagagcat gggcagtgag gacatgctct 540
tcatgctgta cacctcaggg agcaccggaa tgcccaaggg catcgtccat acccaggcag 600
gctacctgct ctatgccgcc ctgactcaca agcttgtgtt tgaccaccag ccaggtgaca 660
tctttggctg tgtggccgac atcggttgga ttacaggaca cagctacgtg gtgtatgggc 720
ctctctgcaa tggtgccacc agcgtccttt ttgagagcac cccagtttat cccaatgctg 780
gtcggtactg ggagacagta gagaggttga agatcaatca gttctatggc gccccaacgg 840
ctgtccggct gttgctgaaa tacggtgatg cctgggtgaa gaagtatgat cgctcctccc 900
tgcggaccct ggggtcagtg ggagagccca tcaactgtga ggcctgggag tggcttcaca 960
gggtggtggg ggacagcagg tgcacgctgg tggacacctg gtggcagaca gaaacaggtg 1020
gcatctgcat cgcaccacgg ccctcggaag aaggggcgga aatcctccct gccatggcga 1080
tgaggccctt ctttggcatc gtccccgtcc tcatggatga gaagggcagc gtcgtggagg 1140
gcagcaacgt ctccggggcc ctgtgcatct cccaggcctg gccgggcatg gccaggacca 1200
tctatggcga ccaccagcga tttgtggacg cctacttcaa ggcctaccca ggctattact 1260
tcactggaga cggggcttac cgaactgagg gcggctatta ccagatcaca gggcggatgg 1320
atgatgtcat caacatcagt ggccaccggc tggggaccgc agagattgag gacgccatcg 1380
ccgaccaccc tgcagtacca gaaagtgctg tcattggcta cccccacgac atcaaaggag 1440
aagctgcctt tgccttcatt gtggtgaaag atagtgcggg tgactcagat gtggtggtgc 1500
aggagctcaa gtccatggtg gccaccaaga tcgccaaata tgctgtgcct gatgagatcc 1560
tggtggtgaa acgtcttcca aaaaccaggt ctgggaaggt catgcggcgg ctcctgagga 1620
agatcatcac tagtgaggcc caggagctgg gagacactac caccttggag gaccccagca 1680
tcatcgcaga gatcctgagt gtctaccaga agtgcaagga caagcaggct gctgctaagt 1740
gagctggcac cttgtggggc tcttgggatg ggcgggcacc caagccctgg cttgtccttc 1800
ccagaaggta cccctgaggt tggcgtcttc ctacgtccca gaagcagccc ccaccccaca 1860
catgacccac accgccctca cgtgaagctg ggctgagagc cctttctccc atccattgga 1920
ggtcccagga gtgtcaccca tggagaggct atgcgacatg gctagggctg gttctgccat 1980
ctgagtttgg tttcctggaa tgaaaaggca ttgccatctc cattcctctg ccctcttgag 2040
ccagcacagg aaggtgaggc cctgggatag cgcgcctgct cagataacac agagctagtt 2100
agctagtagc aaccgtgttt tctccagatc tgtctagata caaaggtcag aaatcttatt 2160
tttatacttt tatattgtgg aagaacagca tgcaacactc acatgtagtg tgtggattta 2220
cttgaacatg ttctttttaa catgtagtta tgaaaatctc ctttttttgcc tctactggtg 2280
aggaaacatg aggatcagag gccacatttt taattattgt tagtgtattt ggaagtctga 2340
attggagatg tttgtacctc tgtctaaaca gttcccttga gaacttccaa gcctccggca 2400
tctttttcctg gtgagtgttt ctcctgtgct tggttgtgta taatggagct aactcctaag 2460
cggtggggtg aatgtggccg ccttagttct gaagctactc cagttatgtt ctgtttcttc 2520
aagctgtgat ccagaaagat ttttgtgccc ccagatgcct cttgatagga gaggcaacat 2580
actccaaata gttgggttct tcagggaagc tattagaaac tcaggtgact tgttagagca 2640
ctaacttggt cagagccaaa tcctggcaaa cgctgcctga ccttcactct gtggttgggg 2700
cagtgagaac cactgaggtc caatgatgag acttggaggt ctggatccag tctctctttg 2760
ttttaatgtg acttaggtgc tgtcaacatt agcaagataa tggaaatcac gacgccagtg 2820
ggtgcttacc tccctgctag gcatgcaggg gctggcggtt ggcaggggaa ggaggcccag 2880
tgagccgggt cccttagggg agggagagtt tgtcctcttt gccccacagt ctacccttca 2940
gggccttgtg gcagtgccag tgttcggggg gtgtctgggc cactgagtac ccactcggtc 3000
gtggttgtgc tggcctcttg ggtgagtgaa cctgtgaagc ccaggaggtg gtgttggctg 3060
cagggtacac aaatactgag tggtggtctt ttgttacagg cttagcaaca aagctgtgcc 3120
ctgggcatgg ggggctgtag tgtagctaca gttgtgcgtt tgtgaaatgg cttagctttc 3180
catgttgctg agaggaacct ggacatggtc ccgggcatct gaatgatctg taggggaggg 3240
agttcaaata aagctttatt ttgttccaaa aaaaaaaaaa aaaaaaaaaa           3290
```

<210> 52
<211> 518
<212> PRT
<213> Homo sapiens

<400> 52

```
Met Pro Val Ser Pro Leu Ala Val Ala Ala Met Leu Ala Cys Ala Arg
 1               5                  10                  15

Ile Gly Ala Val His Thr Val Ile Phe Ala Gly Phe Ser Ala Glu Ser
```

```
            20                  25                  30

Leu Ala Gly Arg Ile Asn Asp Ala Lys Cys Lys Val Val Ile Thr Phe
        35                  40                  45

Asn Gln Gly Leu Arg Gly Gly Arg Val Val Glu Leu Lys Lys Ile Val
    50                  55                  60

Asp Glu Ala Val Lys His Cys Pro Thr Val Gln His Val Leu Val Ala
65                  70                  75                  80

His Arg Thr Asp Asn Lys Val His Met Gly Asp Leu Asp Val Pro Leu
                85                  90                  95

Glu Gln Glu Met Ala Lys Glu Asp Pro Val Cys Ala Pro Glu Ser Met
            100                 105                 110

Gly Ser Glu Asp Met Leu Phe Met Leu Tyr Thr Ser Gly Ser Thr Gly
        115                 120                 125

Met Pro Lys Gly Ile Val His Thr Gln Ala Gly Tyr Leu Leu Tyr Ala
    130                 135                 140

Ala Leu Thr His Lys Leu Val Phe Asp His Gln Pro Gly Asp Ile Phe
145                 150                 155                 160

Gly Cys Val Ala Asp Ile Gly Trp Ile Thr Gly His Ser Tyr Val Val
                165                 170                 175

Tyr Gly Pro Leu Cys Asn Gly Ala Thr Ser Val Leu Phe Glu Ser Thr
            180                 185                 190

Pro Val Tyr Pro Asn Ala Gly Arg Tyr Trp Glu Thr Val Glu Arg Leu
        195                 200                 205

Lys Ile Asn Gln Phe Tyr Gly Ala Pro Thr Ala Val Arg Leu Leu Leu
    210                 215                 220

Lys Tyr Gly Asp Ala Trp Val Lys Lys Tyr Asp Arg Ser Ser Leu Arg
225                 230                 235                 240

Thr Leu Gly Ser Val Gly Glu Pro Ile Asn Cys Glu Ala Trp Glu Trp
                245                 250                 255

Leu His Arg Val Val Gly Asp Ser Arg Cys Thr Leu Val Asp Thr Trp
            260                 265                 270

Trp Gln Thr Glu Thr Gly Gly Ile Cys Ile Ala Pro Arg Pro Ser Glu
        275                 280                 285

Glu Gly Ala Glu Ile Leu Pro Ala Met Ala Met Arg Pro Phe Phe Gly
    290                 295                 300

Ile Val Pro Val Leu Met Asp Glu Lys Gly Ser Val Val Glu Gly Ser
305                 310                 315                 320

Asn Val Ser Gly Ala Leu Cys Ile Ser Gln Ala Trp Pro Gly Met Ala
                325                 330                 335

Arg Thr Ile Tyr Gly Asp His Gln Arg Phe Val Asp Ala Tyr Phe Lys
```

340 345 350

Ala Tyr Pro Gly Tyr Tyr Phe Thr Gly Asp Gly Ala Tyr Arg Thr Glu
355 360 365

Gly Gly Tyr Tyr Gln Ile Thr Gly Arg Met Asp Asp Val Ile Asn Ile
370 375 380

Ser Gly His Arg Leu Gly Thr Ala Glu Ile Glu Asp Ala Ile Ala Asp
385 390 395 400

His Pro Ala Val Pro Glu Ser Ala Val Ile Gly Tyr Pro His Asp Ile
405 410 415

Lys Gly Glu Ala Ala Phe Ala Phe Ile Val Val Lys Asp Ser Ala Gly
420 425 430

Asp Ser Asp Val Val Val Gln Glu Leu Lys Ser Met Val Ala Thr Lys
435 440 445

Ile Ala Lys Tyr Ala Val Pro Asp Glu Ile Leu Val Val Lys Arg Leu
450 455 460

Pro Lys Thr Arg Ser Gly Lys Val Met Arg Arg Leu Leu Arg Lys Ile
465 470 475 480

Ile Thr Ser Glu Ala Gln Glu Leu Gly Asp Thr Thr Thr Leu Glu Asp
485 490 495

Pro Ser Ile Ile Ala Glu Ile Leu Ser Val Tyr Gln Lys Cys Lys Asp
500 505 510

Lys Gln Ala Ala Ala Lys
515

<210> 53
<211> 1467
<212> DNA
<213> Homo sapiens

<400> 53
tcgcctgaac aaggaccatg ctgtcctgca cgctgggtct gaccgtctgc cctctctccc 60
cagcaccaag cgtgaccttg gctgtggcgc tcaacggcca gctccggcgg cccctctgct 120
gctcctcggc tttcccggaa gtgggagagc ctgcctggcc tcggcctttg tccagcgacc 180
aggctctgtc cccgagaagc tacggccgac ctgggtctgg tgttgggacg catggaccgg 240
gctggggagg tgcacagagt gatgttaact ttttcccgtg tgtagatatg tacagccaaa 300
gggtcgtgta aatgttctgc aaaagtgggt ctatacagag tgaaagctat ttattttgtg 360
cagagaaaaa agtctggagg gatggaacct tcagggttta ttcatattta agatgtagct 420
ttttgttgtt tcaggcatta tgtataaagc aacgattatt ttatggacca agttttcatg 480
taactgttgc agtgaaagtg caatatctga ccccccctgct cccagcagga agttgcttgg 540
cccgacaatc acagcccctg tcaggggccc tgtggccagt gcctcctcct ctcttggccc 600
caccttatcc tgtcttgcct gctgcctggg agaccagcca tccagagaag cacctggaag 660
agtctcgggc cctcctgcaa taaaggccgg gaggccctgt gggcagtggg ctcagcctct 720
ccccaggggg gcagctcccc cacggctcct cactccccgc ctgcctgccc agccgccagc 780
catgccaagg acaacagcaa tagtcccctg gggctctccc agcggccctc agccatagat 840
ggcaaggtgg gcagcctgcc cccccatggg aagtctcttc tgtatccagg tctgctttcc 900
acctcccttc agattccttt tggcacattc tcctcttgag gaagtaccag tctttctgaa 960
actaagagag ggagggcagc gtcctttaaa aataccaaaa atgtttacag agttgggtgc 1020
tgagctgcag ggctcaggcc tgaccagtca taaccaaagg gtgaggcagg ccttgctgac 1080

tgccaccccc caggcctgtt agaatagaag ccttagtccc actcccacca cacccccacg 1140
ccccaccacc tgccttctct ttgatttcta aagagggatt cagcagagac cccccacccc 1200
tccctggctc ggtctgagtc ccactgccca ccccatcaca gccttcacgt ctcagcccct 1260
cccgtctggt ctgtccgtgt gccgtctgtt tctctgggcc atgtgtgagc agtgtcccca 1320
tctccccatc cgtccctgct gtccccgcat cattgggcct gagtgtgctc tgtatacaac 1380
gtcatgtctg ttacaccaat taaagaagcg ggaaggcttc aaaaaaaaaa aaaaaaaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaa 1467

<210> 54
<211> 132
<212> PRT
<213> Homo sapiens

<400> 54
Met Tyr Lys Ala Thr Ile Ile Leu Trp Thr Lys Phe Ser Cys Asn Cys
1 5 10 15

Cys Ser Glu Ser Ala Ile Ser Asp Pro Pro Ala Pro Ser Arg Lys Leu
20 25 30

Leu Gly Pro Thr Ile Thr Ala Pro Val Arg Gly Pro Val Ala Ser Ala
35 40 45

Ser Ser Ser Leu Gly Pro Thr Leu Ser Cys Leu Ala Cys Cys Leu Gly
50 55 60

Asp Gln Pro Ser Arg Glu Ala Pro Gly Arg Val Ser Gly Pro Pro Ala
65 70 75 80

Ile Lys Ala Gly Arg Pro Cys Gly Gln Trp Ala Gln Pro Leu Pro Arg
85 90 95

Gly Ala Ala Pro Pro Arg Leu Leu Thr Pro Arg Leu Pro Ala Gln Pro
100 105 110

Pro Ala Met Pro Arg Thr Thr Ala Ile Val Pro Trp Gly Ser Pro Ser
115 120 125

Gly Pro Gln Pro
130

<210> 55
<211> 943
<212> DNA
<213> Homo sapiens

<400> 55
tatacttgct taagcaatct tgatttgagt aagggtcttg atttgtgcta ttatgttctg 60
ttagttttgg catgaatata ctaaagcttt tttttttttt tctagcatgt gttttctcct 120
ctttggttct ctttgtattt actacttttc tctttttctt gtgttttttt tttcctgttt 180
ttgttttgtt tggtgttttg ttcctgtctt cattgtttca ggtatttctt taccccctctg 240
gattccccac gggctggatc gagatggtcc agttatgccc agctccttcc tcctcctcct 300
cctcctctgg tagagcactc ttgcgatgct gacactgcca acctccagta tcctcaccct 360
cgcagacgat atctctctcg gcctcttaat cccttacctg agaatgaagg gatttaaaac 420
actgatttaa cattgaaagg ccttattcaa gtgcttgtaa atgctttcat ttctggctgc 480
tttttgtttt tcattttctt tcagaagatt tttctaactt agggtctgtc ttgcatgtat 540
tacaaccaga atacagtgtt tggaacctaa atctgtttgt gcgtctgcat caaaggaaca 600
tttgcttcac tgggtgataa cctttgatga aatgagatat gtccaagtaa cgttaactgt 660
gaagttacac acagtagctg acttcaaagt gcctgttctg taaattttat tttaaactgt 720

taccatagtc ttaagttgtt tatgctttat cagactggct aatgtgaaag cataatatta 780
tgaagtttat tctgccttat gagaccttaa aaaatggatt tcattttaca ggctaatgtt 840
gtaactgact agtatgtaaa ataaatcatt cctgtgtata aagcagcaaa acctaaaaaa 900
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 943

<210> 56
<211> 86
<212> PRT
<213> Homo sapiens

<400> 56
Met Asn Ile Leu Lys Leu Phe Phe Phe Phe Leu Ala Cys Val Phe Ser
1 5 10 15

Ser Leu Val Leu Phe Val Phe Thr Thr Phe Leu Phe Phe Leu Cys Phe
20 25 30

Phe Phe Pro Val Phe Val Leu Phe Gly Val Leu Phe Leu Ser Ser Leu
35 40 45

Phe Gln Val Phe Leu Tyr Pro Ser Gly Phe Pro Thr Gly Trp Ile Glu
50 55 60

Met Val Gln Leu Cys Pro Ala Pro Ser Ser Ser Ser Ser Ser Ser Gly
65 70 75 80

Arg Ala Leu Leu Arg Cys
85

<210> 57
<211> 1032
<212> DNA
<213> Homo sapiens

<400> 57
aaaacgaatt gattaatgaa gagttgggaa tagcttatcc aatcattgat gggatcccta 60
atatgatacc acaggcagct aggatgacac gtcaaagtaa gaagcaagaa gaagtggagc 120
agcgctagtt cataatttaa aaaaattaaa aaaacgcaac agccaacttt tcttaatacc 180
atataccttt taaaacacag tggcaggtaa taagtggaag agaagaatgt ttctgtctct 240
tcctacgttg actgttctta ttccactggt ttctttagca ggactgttct actcagcctc 300
tgtggaagaa aacttcccac agggctgcac tagcacagcc agcctttgct tttacagcct 360
gctcttgcct attaccatac cagtgtatgt attcttccac ctttggactt ggatgggtat 420
taaactcttc aggcataatt gatgcaacta gagtcaatat gctgtatata ttaatgatag 480
ctcttgggca tcgatctctg aaagctcaaa tggatggaat ttagtttgcg ggaaagaggc 540
tttgctttgc gcatatcagg cttaggactg tgggaggctt aagttgcaga tgcttctttt 600
attgtactct tgttctgccc ttgtttttttg aaggctctga cttataactg ctgtatcaga 660
agaaacattt tgacagtgtc ttggttggag atgaacatcc ctaattgaca tgtgatgact 720
atttcttatt ccattcatct aagagtcatt gaaattttgt tttgcttgtt tgtttagctt 780
caaggtcttt ggtaaagtca catgttaagg atgactgaaa taattccaaa ggagtgatgt 840
tggaatagtc cctctaaggg agagaaatgc atttgaacga atgtgatata aaaccacata 900
atcaaataga aacttcatgt acttacaaaa actgagtttg taaaattacc ttcatttctt 960
tgacattaaa tgcttatatt agcaataaac atgttgacac tttcctataa aaaaaaaaaa 1020
aaaaaaaaaa aa 1032

<210> 58
<211> 71
<212> PRT
<213> Homo sapiens

<400> 58
Met Phe Leu Ser Leu Pro Thr Leu Thr Val Leu Ile Pro Leu Val Ser
1 5 10 15

Leu Ala Gly Leu Phe Tyr Ser Ala Ser Val Glu Glu Asn Phe Pro Gln
20 25 30

Gly Cys Thr Ser Thr Ala Ser Leu Cys Phe Tyr Ser Leu Leu Leu Pro
35 40 45

Ile Thr Ile Pro Val Tyr Val Phe Phe His Leu Trp Thr Trp Met Gly
50 55 60

Ile Lys Leu Phe Arg His Asn
65 70

<210> 59
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 59
gtagcatttg tctccttcct tcaatttgtt aacacatcag atagtagatt tttcgtagta 60
agaatgaaat gtttttactt ctcctttaat attttatggt gaatgtcaga gcctccatat 120
tggaaattaa aaggcacctt ttactgcatt cttcctgtgc tttgtctagg tcctttctag 180
agccttcagg aatcggtttg tggaattgca ctttgatgag ttacctagct ccgagttgga 240
aacaatcttg cacaagcggt gtagtttgcc accctcctat tgcagcaagt tggttaaagt 300
catgctggat cttcaggtac ttagtttcaa atggaatgta ttgattatac ttggtgatca 360
aaatttcatg gcttcttttg ttagaaaaaa gaatctgtct gttgatgtat ttttccaagt 420
agagattttt ttttattttt tattgttttt aattttttta ttatttattt tttgcaagac 480
acagtctcac tctactctcc tggctggagt gtagtggcac aatcatagct cattgcagcc 540
ttgacctcct gggctcaggt gatcctccca tctctgacta ctcactcctt agtagctggg 600
accacagatg tgcaccgtca tgcccggcta cattttttttt tttgtagaga caaggtttcg 660
ccatgttgcc ccggctggtc tcgaactcct gggctcaagg gatccaccca ccttgatctc 720
ccaaagtttt gggattatag gtgtgaacca cagttcttgg ccttcaagta gaggtctttt 780
aaatgcttcc caataatata tatttttagt tttttttttt aatcaatcaa caattttaca 840
tcattaaaat ttttctgata tttacatatg aggatttgt atttgtgtat aatattgaag 900
cattttgttt agaatgtaat ttggcttagg gaaaactggt ttttggtttt taaatggata 960
tagtccttga atggacataa ttaaagagat ccattctttg tggctccccc tagtcaactg 1020
caaagctaca gctgatcttt aaaaattcca tttatcttat ggggttaaaa gttttcttta 1080
tcagaaagta tacattgtca aacttctttt tagaaagcta ataataatga agactcctac 1140
cattatggtt ccacattgtt tcactaatct tcctgcatct ttgccaccat ttgcattact 1200
ttttgtttgt tttttgagac agagcctcac tctgtcgcca ggctggagtg cagtggcgct 1260
atctcagctc actgcaacct ccgcctcccg ggttcaagca attcccctgc ctcagcctcc 1320
tgagtagctg cgactatagg cgtgcaccac caggcttggc taattttttg tctctataaa 1380
aaatttttaa agttggccag ggtgatggc tctgcctgta gtcccagcta ctcgaaaggc 1440
ccaggtggga ggactgcttg agcctaggtg ttccaggctg cagggagctg tgatagctcc 1500
actgcactcc accctgtgta ataaagggag actgtatctc aaaaaaaaaa aaaaaaaaaa 1560
aaaa 1564

<210> 60
<211> 82
<212> PRT
<213> Homo sapiens

<400> 60
Met Val Asn Val Arg Ala Ser Ile Leu Glu Ile Lys Arg His Leu Leu
1 5 10 15

Leu His Ser Ser Cys Ala Leu Ser Arg Ser Phe Leu Glu Pro Ser Gly
20 25 30

Ile Gly Leu Trp Asn Cys Thr Leu Met Ser Tyr Leu Ala Pro Ser Trp
35 40 45

Lys Gln Ser Cys Thr Ser Gly Val Val Cys His Pro Pro Ile Ala Ala
50 55 60

Ser Trp Leu Lys Ser Cys Trp Ile Phe Arg Tyr Leu Val Ser Asn Gly
65 70 75 80

Met Tyr

<210> 61
<211> 2800
<212> DNA
<213> Homo sapiens

<400> 61
taatagatta ttatcaacta gagatattta taaatgaagt atatactttt aaaacatgta 60
agttatacta atttgtgtt taatttcata tgttttcatg taatgaaaat tctatttttt 120
ttagaattgg ttttgttttt attctattat cctttatttc cagttgtcaa actttaaatg 180
gctatgtctg cattctaata acactgttca gtctgttatg gaaaaggaga actagggaac 240
aaatgttgct cagggctggt gtcagtgaga aaaatttatc aatgcttttt aatgtgtttt 300
tacccttgcc tcactctgtg tgtgtcactt tctataatat aaagaaatac tataatattt 360
ctagaatctg gaactgtcac catgatgaat ggccctttca atgcatagtt acagaaattc 420
ctgaagattc cccaggactt caatttcatt ggtttttatt tgcagttttt agttgctgta 480
attgttgctg tttccagtct aaaggacctc ctttggtaaa ggtgaacaag acctctcccc 540
tatgctaccc agccagattt tgtgtgtgta atgggctggc ccaagagtgt tcttttactt 600
agaactcctt ttgattttgc ttttctctgc cctagaaat tttagggaca aagacatttt 660
ggaaattgtc agttactttt agaaagaaaa cactgcagaa atatttaaca gattacttct 720
tgataaaatt taaatgggat tatatgaatt tgtaatgcca attgaaaata ttatatacac 780
aaaatttgct attttcactt aaagtaagca tttttaaagg atttatttta gaatacaatc 840
tatgcaatcc tcgaactcag tgtgcttttc cctgacagga tatataaaaa ggtagattag 900
gtcaacccctc ctttaagctt cctctcccct caccttttct tttcactgta tataaacggt 960
actttctgtg attcatacca acagtcctaa actgtcattt tctaaatctg ggatttaaaa 1020
tctttaaaca atatttaaaa tcttgatttt ttttaaatgt cagcagatac aatttggaag 1080
attgcatctg tgtagaagta atgcaggtac aagatctaga gtttttcctt agactcttta 1140
gtcttttctg aattaaagaa taagtgctct taaatccata ttttatcctg tcaaagtctg 1200
aaatgtgttc attgatgatt tggtgacatc taaaaaattg tatttagttg gcttggctca 1260
cccctcttaa aaatacttag ccatctcttg gtgggatgtg gtgggggtat taaggtctca 1320
gagttattta ttttctcacc taatttcaaa cctttataaa cttggggttt tgttgttgat 1380
ggtggtagta ttttttgtta agttgtttaa aaggctgact tgattggagc ctcctctact 1440
ttttcttgag ggttgcaagt attgtatggt gggggagggg ggccttaagg caaactgtct 1500
aaaaagtgac tatccaatta atttaactag taaattagta agaattattc ttagtattca 1560
ttcagagttt aagatgtgaa aaatctgcac tttgtttatc actctaaatg taaagaactt 1620
tttgatagtg ttatttcacc actccctcag ttaaaggcta ttatttaaac tgtttactgg 1680
agaaaatcct cgctcatgtc catttattgt ttttttctgt actgtgattt gtttcaagct 1740
taggaaaact agtatattag agtatgttct aggaaattaa aagatctggt tagagtaaaa 1800
agttcttttt aaggttctta actaattttt tcacaactaa gaaaataaat gaagtattct 1860
taggctgaaa ttcatcttat tttatcataa attagattgt aggggcagcc tacattttttg 1920
tgtatgtgtt tttatttctt aaatgattgt gtgagcctgg tgacatttta tggttcttgt 1980
gatctaaact gtttttccaa ttcacatctt ttgttgtgaa gtgatattat actagagtac 2040
tgtttgcatt gtaaaaatgc tttgctggtg ctctggcatt ttgtctttat ctcatcacct 2100
aatttaaaaa cccagcactt gataatataa ctgacagaaa tgattgtacc cactgatgaa 2160
gtaatgaaaa tgaagaaaag gaaaatattc cttccttcaa tggcgtaagt ttatttttta 2220
cttaagtggc atctatgtaa gttagacaaa ctatatatta aaattggtaa actttgaatg 2280

tttctcctgt tttgattctt agattatgag gaggatcaga cagaataaga ctccacactt 2340
ttgaaatttg ataagtcaaa acgttttatt ttgacatttt taacattgtg aattattcga 2400
tatttgtaat ctatgtatat gaaactctgc catgtttttc aactttgcct atgtgccact 2460
gtatataaga aaggacagct atttggatct tcatcagcat tgccttcagc tgaaaatttg 2520
ggaacagttc acagtaaacc tctcagtagt ttgcaaactg aggtacctgc agaaaccata 2580
gctactcacc aaaatacaag attaggtgca tggtatcgtg gaaattattt ggtaaaaaaa 2640
cacacacaca aatctatgtg tactgtattt taaggaatat ctacaggtgc agctttgatt 2700
ttgaacagaa ttccaaataa tttactgttg tacccaccag aatctagaaa atgtgaatta 2760
aagtacatgt ttctgcaaaa aaaaaaaaaa aaaaaaaaa 2800

<210> 62
<211> 170
<212> PRT
<213> Homo sapiens

<400> 62
Met Phe Ser Cys Asn Glu Asn Ser Ile Phe Phe Arg Ile Gly Phe Val
1 5 10 15

Phe Ile Leu Leu Ser Phe Ile Ser Ser Cys Gln Thr Leu Asn Gly Tyr
20 25 30

Val Cys Ile Leu Ile Thr Leu Phe Ser Leu Leu Trp Lys Arg Arg Thr
35 40 45

Arg Glu Gln Met Leu Leu Arg Ala Gly Val Ser Glu Lys Asn Leu Ser
50 55 60

Met Leu Phe Asn Val Phe Leu Pro Leu Pro His Ser Val Cys Val Thr
65 70 75 80

Phe Tyr Asn Ile Lys Lys Tyr Tyr Asn Ile Ser Arg Ile Trp Asn Cys
85 90 95

His His Asp Glu Trp Pro Phe Gln Cys Ile Val Thr Glu Ile Pro Glu
100 105 110

Asp Ser Pro Gly Leu Gln Phe His Trp Phe Leu Phe Ala Val Phe Ser
115 120 125

Cys Cys Asn Cys Cys Cys Phe Gln Ser Lys Gly Pro Pro Leu Val Lys
130 135 140

Val Asn Lys Thr Ser Pro Leu Cys Tyr Pro Ala Arg Phe Cys Val Cys
145 150 155 160

Asn Gly Leu Ala Gln Glu Cys Ser Phe Thr
165 170

<210> 63
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 63
acaccatgtc atgccctttg ccactgttga tttcagccat agctgcagtg ggtagttcca 60
tgcaaactca cgctcgagcc agttttgctg cagggccttc tcagaagact tctcagccca 120
tttggcccag gatcaacaca gcccagaagt gcaggggcat taccacgcca ggggcaatcc 180
tccagcagtg ggagatacaa gcctatggat gaaggttccc acctcccatc actcagatga 240

```
gaaacaccaa gaggcttctt gtacctttct cagaggccac agcaggatca atcccccatt 300
gcacacagca gccatctcaa taatgcacca ttctattagt gggtatatgc ataacagggt 360
attccttggt gcctctcttg gtttttcaag ctcagcaata gtggagtggt tgcacagcca 420
ggggctagca atggaagcac acaaaagggc ttgaactgct caccaagtta ctgggttact 480
tcacctggta aacaacctaa atcacatagg cgccactaag agtaggagaa atctaaaatg 540
ggtaatgggg aagggagatg aggaattaat tacagctggc ttaatcagaa ctgcctgcat 600
ccgctggtac tttagcatgg gacatgtact tcatgttgcc caggctggcc tcgaactcct 660
gggctcaagc gatcctctca cctcagcctc tggagtagct gggactatag gcacatgcca 720
ccatattcag caggacatat acttttaaaa gtgtgggatc tgctgtcacc ttgaggatgt 780
actaactggg ttgacttcat gtagggcatg ggtagatctg agcagggcaa agtagactgc 840
aggagatgtt cgggatgccc cacaccatgt catgcccttt gccactgttg atttcagcca 900
tagctgcagt gggtagttcc atgcaaactc acgctcgagc cagttttgct gcagggcctt 960
ctcagaagac ttctcagccc atttggtcca ggattttcct cccacttaaa gtaactgctc 1020
ccaagtcctg ccccatgttc tactttcagg agttcccaaa ctaaggcaat agctgcacct 1080
gcaaagaaag cgactacttg ttaatatgtg atataatcca gaaaagcaag agtccaccca 1140
aagtcagaag agaagaattc agaagagtaa ggtgggtgtg ggcatatgat acgtatgagg 1200
gggcatttga taacttcaac ctaccaagtg cagttcattc agtaagccag taatataggg 1260
ttttagagct gacaatgtga ggtataatat acaaaagctt agaaaggcat agggagacat 1320
ctatcttttt cctttgcttt gagggcatgt gcttgcatca gctctgtgtg tgtgtgtgtg 1380
tgtgtgtgtg tgtgtataca cacacataca ctagactata aaaagaaatc acgacatcca 1440
tacggaggaa cctgggtatt tgaatcccag aaactttctc aaggcctcac tagggaaaga 1500
tagttcagtt acaagccaaa gactcaagag gaaaaagccc ctggagtgaa taaatagtct 1560
gataaaccta gacatatgtg gtaactgcag aaataagtcc tttttcattt atagagggag 1620
agaagttgca tatattaatc atgtctgctc ttgcccccac tttcaggaac cacttatatg 1680
ccttatgaaa catcaatgtt ccatgaaaca cagtttgaaa acctgagcta acctctcacc 1740
tttcttctag agcgtctcca cttggtcatc tctaacagac cggaccccgc cactttgcta 1800
ggatatccca gaggagacca gagcagaatt ccctgtgaag atattgcaaa tgctgcacca 1860
ctttgacaca gacgaatatt gccttaatgc tttctcattg cagctccatt ctcattcctc 1920
ttgttctaat ctcactggga acagtaagaa gctgccatca ttttatgtta tacttttaca 1980
tactttaagg ttattactga ttaatgagaa ttaaaggaag ctgagaatat ataaaaaaaa 2040
aaaaaaaaaa aaaaaa                                                 2056
```

<210> 64
<211> 81
<212> PRT
<213> Homo sapiens

<400> 64

```
Met Lys Val Pro Thr Ser His His Ser Asp Glu Lys His Gln Glu Ala
  1               5                  10                  15

Ser Cys Thr Phe Leu Arg Gly His Ser Arg Ile Asn Pro Pro Leu His
             20                  25                  30

Thr Ala Ala Ile Ser Ile Met His His Ser Ile Ser Gly Tyr Met His
         35                  40                  45

Asn Arg Val Phe Leu Gly Ala Ser Leu Gly Phe Ser Ser Ser Ala Ile
     50                  55                  60

Val Glu Trp Leu His Ser Gln Gly Leu Ala Met Glu Ala His Lys Arg
 65                  70                  75                  80

Ala
```

<210> 65
<211> 581
<212> DNA

<213> Homo sapiens

<400> 65
aaaatatata tgaatagata aatataacta atgtgcgtga gaatgggcct ggcacacctg 60
gggtgctcgg gggtagggct gccatgctgc agagctgatg gagtgatgtt gtgggcacaa 120
ggcatctgtc agctgcctcc tttaacagcc atgccttctg gaatctggaa gaggacacca 180
ctcctgcagt cactgggcag ccacatagca gctgcaggtc ccaggagggc ctgaggtcaa 240
agctgtggaa ggccctcttg gtatcagggc tctctcccca tggcctcttc cccacctctg 300
attgctggtt gtggccccat agctcatcac ccctgtctcc tgctgaatgt gcagggctga 360
tgtggcactg aggagctgac tttggtcaaa ggccaggctc tgcccagcag gggacttgac 420
tgccctgggc gccctgcccc tcccgctgcg tgtccaggtc caaagtggag agcctgcctt 480
tgggtttagt tcccgaatca gaatcccatc tcaccagggc gaaattttaa tttaaaaact 540
taaaaagaga cttttctaaa aaaaaaaaaa aaaaaaaaaa a 581

<210> 66
<211> 67
<212> PRT
<213> Homo sapiens

<400> 66
Met Cys Val Arg Met Gly Leu Ala His Leu Gly Cys Ser Gly Val Gly
1 5 10 15

Leu Pro Cys Cys Arg Ala Asp Gly Val Met Leu Trp Ala Gln Gly Ile
20 25 30

Cys Gln Leu Pro Pro Leu Thr Ala Met Pro Ser Gly Ile Trp Lys Arg
35 40 45

Thr Pro Leu Leu Gln Ser Leu Gly Ser His Ile Ala Ala Ala Gly Pro
50 55 60

Arg Arg Ala
65

<210> 67
<211> 1916
<212> DNA
<213> Homo sapiens

<400> 67
gaaggagaga cggctggcca ccatgcacgg ctcctgcagt ttcctgatgc ttctgctgcc 60
gctactgcta ctgctggtgg ccaccacagg ccccgttgga gccctcacag atgaggagaa 120
acgtttgatg gtggagctgc acaacctcta ccgggcccag gtatccccga cggcctcaga 180
catgctgcac atgagatggg acgaggagct ggccgccttc gccaaggcct acgcacggca 240
gtgcgtgtgg ggccacaaca aggagcgcgg gcgccgcggc gagaatctgt tcgccatcac 300
agatgaggag ccagttacct tccccaaatc gacccatgtt cctatcccaa aatcagcaga 360
caaagtgaca gacaaaacaa aagtgccctc taggagccca gagaactctc tggaccccaa 420
gatgtccctg acaggggcaa gggaactcct accccatgcc caggaggagg ctgaggctga 480
ggctgagttg cctccttcca gtgaggtctt ggcctcagtt tttccagccc aggacaagcc 540
aggtgagctg caggccacac tggaccacac ggggcacacc tcctccaagt ccctgcccaa 600
tttccccaat acctctgcca ccgctaatgc cacgggtggg cgtgccctgg ctctgcagtc 660
gtccttgcca ggtaaggccc atagcatctg tcccactttc ctcctggctc tggaatgtca 720
gtatcctgcc ccagcatagg tggtatgagc atggtggggc atgcaccctc tgagtaggag 780
cttcctccct ggctgctgcc ccacctcctt gcatggtggg gtgggcggga catcaggcac 840
agctgtctct aggctgaggc aaagcctctt tcttcccaca ggtgcagagg gccctgacaa 900
gcctagcgtc gtgtcagggc tgaactcggg ccctggtcat gtgtggggcc ctctcctggg 960
actactgctc ctgcctcctc tggtgttggc tggaatcttc tgaaggggat accactcaaa 1020
ggcaaggcct ggtgaggggg gccctggcct catacccacc tggattgtct tcctccaagt 1080

gagagaccac agcttcctgg gcaggtcctg ctctgtggcc cagcagcccc ccttcacccc 1140
aacttctggc cagattccag gccagcactc ttgtcctcct gggaggcgtc tacagggcca 1200
gcccctggca ctgccccagg agtgccttgg ctctgggtag gcccatcctt cagctggctg 1260
cagactgttc tgagcggtat ttacatgtgc ccactctcag gttgtcctgt ggccatcagc 1320
ttctctccca gacagaggat ctcaggcttc ccaggaaccc ccgggcccct cccagtcccc 1380
tggcctcttc cttgagccat ctgagtccag gactgttccc cagaagtgcc tcttgccttc 1440
tcagggtgaa gaggtcagct gtcctcctgt catcttcccc accctgtccc cagcccctaa 1500
acaagatact tcttggttaa ggccctccgg aagggaaagg ctacggggca tgtgcctcat 1560
cacaccatcc atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1620
ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg gggtgggag 1680
gatttgaggg agctcactgc ctacctggcc tggggctgtc tgcccacaca gcatgtgcgc 1740
tctccctgag tgcctgtgta gctggggatg gggattccta ggggcagatg aaggacaagc 1800
cccactggag tggggttctt tgagtggggg aggcagggac gagggaagga aagtaactcc 1860
tgactctcca ataaaaacct gtccaacctg tgaaaaaaaa aaaaaaaaaa aaaaaa 1916

<210> 68
<211> 238
<212> PRT
<213> Homo sapiens

<400> 68
Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu Leu
1 5 10 15

Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp Glu Glu
20 25 30

Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala Gln Val Ser
35 40 45

Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp Glu Glu Leu Ala
50 55 60

Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val Trp Gly His Asn Lys
65 70 75 80

Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe Ala Ile Thr Asp Glu Glu
85 90 95

Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile Pro Lys Ser Ala
100 105 110

Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser Arg Ser Pro Glu Asn
115 120 125

Ser Leu Asp Pro Lys Met Ser Leu Thr Gly Ala Arg Glu Leu Leu Pro
130 135 140

His Ala Gln Glu Glu Ala Glu Ala Glu Ala Glu Leu Pro Pro Ser Ser
145 150 155 160

Glu Val Leu Ala Ser Val Phe Pro Ala Gln Asp Lys Pro Gly Glu Leu
165 170 175

Gln Ala Thr Leu Asp His Thr Gly His Thr Ser Ser Lys Ser Leu Pro
180 185 190

Asn Phe Pro Asn Thr Ser Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala
195 200 205

Leu Ala Leu Gln Ser Ser Leu Pro Gly Lys Ala His Ser Ile Cys Pro
210 215 220

Thr Phe Leu Leu Ala Leu Glu Cys Gln Tyr Pro Ala Pro Ala
225 230 235

<210> 69
<211> 2051
<212> DNA
<213> Homo sapiens

<400> 69
gggctcgctg gccgctcctg gaggcggcgg cgggagcgca gggggcgcgc ggcccgggga 60
ctcgcattcc ccggttcccc ctccacccca cgcggcctgg accatggacg ccagatggtg 120
ggcagtggtg gtgctggctg cgttcccctc cctaggggca ggtggggaga ctcccgaagc 180
ccctccggag tcatggaccc agctatggtt cttccgattt gtggtgaatg ctgctggcta 240
tgccagcttt atggtacctg gctacctcct ggtgcagtac ttcaggcgga agaactacct 300
ggagaccggt aggggcctct gctttcccct ggtgaaagct tgtgtgtttg gcaatgagcc 360
caaggcctct gatgaggttc ccctggcgcc ccgaacagag gcggcagaga ccaccccgat 420
gtggcaggcc ctgaagctgc tcttctgtgc cacagggctc caggtgtctt atctgacttg 480
ggtgtgctg caggaaagag tgatgacccg cagctatggg gccacagcca catcaccggg 540
tgagcgcttt acggactcgc agttcctggt gctaatgaac cgagtgctgg cactgattgt 600
ggctggcctc tcctgtgttc tctgcaagca gccccggcat ggggcaccca tgtaccggta 660
ctcctttgcc agcctgtcca atgtgcttag cagctggtgc caatacgaag ctcttaagtt 720
cgtcagcttc cccacccagg tgctggccaa ggcctctaag gtgatccctg tcatgctgat 780
gggaaagctt gtgtctcggc gcagctacga acactgggag tacctgacag ccacactcat 840
ctccattggg gtcagcatgt ttctgctatc cagcggacca gagccccgca gctccccagc 900
caccacactc tcaggcctca tcttactggc aggttatatt gcttttgaca gcttcacctc 960
aaactggcag gatgccctgt ttgcctataa gatgtcatcg gtgcagatga tgtttggggt 1020
caatttcttc tcctgcctct tcacagtggg ctcactgcta gaacaggggg ccctactgga 1080
gggaacccgc ttcatggggc gacacagtga gtttgctgcc catgccctgc tactctccat 1140
ctgctccgca tgtggccagc tcttcatctt ttacaccatt gggcagtttg gggctgccgt 1200
cttcaccatc atcatgaccc tccgccaggc ctttgccatc cttctttcct gccttctcta 1260
tggccacact gtcactgtgg tgggaggggct gggggtggct gtggtctttg ctgccctcct 1320
gctcagagtc tacgcgcggg gccgtctaaa gcaacgggga aagaaggctg tgcctgttga 1380
gtctcctgtg cagaaggttt gagggtggaa agggcctgag ggtgaagtg aaataggacc 1440
ctcccaccat ccccttctgc tgtaacctct gagggagctg gctgaaaggg caaaatgcag 1500
gtgttttctc agtatcacag accagctctg cagcagggga ttggggagcc caggaggcag 1560
ccttcccttt tgccttaagt cacccatctt ccagtaagca gtttattctg agccccgggg 1620
gtagacagtc ctcagtgagg ggttttgggg agtttggggt caagagagca taggtaggtt 1680
ccacagttac tcttcccaca agttccctta agtcttgccc tagctgtgct ctgccacctt 1740
ccagactcac tcccctctgc aaatacctgc atttcttacc ctggtgagaa aagcacaagc 1800
ggtgtaggct ccaatgctgc tttcccagga gggtgaagat ggtgctgtgc tgaggaaagg 1860
ggatgcagag ccctgcccag caccaccacc tcctatgctc ctggatccct aggctctgtt 1920
ccatgagcct gttgcaggtt ttggtacttt agaaatgtaa ctttttgctc ttataatttt 1980
attttattaa attaaattac tgcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040
aaaaaaaaaa a 2051

<210> 70
<211> 432
<212> PRT
<213> Homo sapiens

<400> 70
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
210 215 220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225 230 235 240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
245 250 255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
260 265 270

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
275 280 285

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
290 295 300

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305 310 315 320

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
325 330 335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
340 345 350

```
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
        355                 360                 365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
    370                 375                 380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385                 390                 395                 400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
                405                 410                 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
            420                 425                 430


<210> 71
<211> 2557
<212> DNA
<213> Homo sapiens

<400> 71
tatatgacat tgtccacaga aacaaataca aagattggat caaaggatgg agaaatttta 60
atgcagggca tgaacatcct gatcaaaact catttacttt tgctcccaat ggtgtgcctt 120
tcattactga ggctctgtac gggccaaagt acaccttctt caacaatgtt ttgatgtttt 180
ccccagctgt gtcaaagagc tgcttttctc cctgggtggg tcaggtcaca gaagactgct 240
catcaaaatg gtctaaatac aagcatgacc tggcagctag ttgtcagggg agggtggttg 300
cagcagagga gaaaaatggg gtggttttca tccgaggaga aggtgtggga gcttataacc 360
cccagctcaa cctgaagaat gttcagagga atctcatcct cctacatcca cagctgcttc 420
tccttgtaga ccaaatacac ctgggagagg agagtccctt ggagacagca gcgagcttct 480
tccataatgt ggatgttcct tttgaggaga ctgtggtaga tggtgtccat ggggctttca 540
tcaggcagag agatggtctc tataaaatgt actggatgga cgatactggc tacagcgaga 600
aagcaacctt tgcctcagtg acatatcctc ggggctatcc ctacaacggg acaaactatg 660
tgaatgtcac catgcacctc cgaagtccca tcaccagggc agcttacctc ttcatagggc 720
catctataga tgttcagagc ttcactgtcc acggagactc tcagcaactg gatgtgttca 780
tagccaccag caaacatgcc tacgccacat acctgtggac aggtgaggcc acaggacagt 840
ctgcctttgc acaggtcatt gctgatcgtc acaaaattct gtttgaccgg aattcagcca 900
tcaagagcag cattgtccct gaggtgaagg actatgctgc tattgtggaa cagaacttgc 960
agcattttaa accagtgttt cagctgctgg agaagcagat actgtcccga gtccggaaca 1020
cagctagctt taggaagact gctgaacgcc tgctgagatt ttcagataag agacagactg 1080
aggaggccat tgacaggatt tttgccatat cacagcaaca gcagcagcaa agcaagtcaa 1140
agaaaaaccg aagggcaggc aaacgctata aatttgtgga tgctgtccct gatatttttg 1200
cacagattga agtcaatgag aaaaagatta gacagaaagc tcagattttg gcacagaaag 1260
aactacccat agatgaagat gaagaaatga aagacctttt agattttgca gatgtaacat 1320
acgagaaaca taaaaatggg ggcttgatta aaggccggtt tggacaggca cggatggtga 1380
caactacaca cagcagggcc ccatcactgt ctgcttccta taccaggttg ttcctgattc 1440
tgaacattgc tatttctttt gtcatgttgg caatgcaact gacttatttc cagagggccc 1500
agagcctaca tggccaaaga tgtctttatg cagttcttct catagatagc tgtattttat 1560
tatggttgta ctcttcttgt tcccaatcac agtgttagca ctgaagctat aaattacctg 1620
gtcattttgt gatcacaaga gtctatgcaa aaaaaaaaat ttctttaccc cagattatca 1680
gatttttttc cctcagattc attttaacaa attaagggaa gatattttga cacaagaaag 1740
caggaacgtg gagaaattgg agcaggaaaa gaaattatca aagcaataga aatagcttgg 1800
tggtcctatg gtgtttttgg aagtatttgg cattgctaat tgagcagtcc atatagtact 1860
acttttagaa gaaacaaaaa gtctattttt taaagtaatg ttttttctta tgagaaaaag 1920
gtttagatag aattgggttt tattaatatt aatttaatgc tattagcaat ttccatatac 1980
tatattgtgg aaaagactga agaatacaat tctgagaaat ataaaaaaat tttaatggta 2040
tactcatgtt gaaagataaa tgttgctaag tcctggtatg atggtgtgag cttccttggg 2100
gaagtacttc ttgagttatg taactaacag gatgttttac tacagatctg gatggctatt 2160
cagataacat ggcaaaaaat gatagcagaa gatcattaaa aacttaaaat atattttatt 2220
```

agaaaacatt tatctatgaa tgaatatttc cttgatgctg gtctctgcac acatatgctt 2280
ggttacttgc atgcattcat tggttgttca ataagtgaga tgattacaga taatactgta 2340
ttttccttat atggaaaacc gttatagacc caataacaac taaacctttc aaaagaaaat 2400
atttctatt atgaatgttg attttcatac caaagaagat ggagagtcta aaatttggat 2460
atgattctta tgttttttta atagaaaacc ttcttcaagt ttattttcct aaataaacat 2520
cataattgtg aaaaaaaaaa aaaaaaaaaa aaaaaaa 2557

<210> 72
<211> 474
<212> PRT
<213> Homo sapiens

<400> 72
Met Phe Ser Pro Ala Val Ser Lys Ser Cys Phe Ser Pro Trp Val Gly
1   5   10   15

Gln Val Thr Glu Asp Cys Ser Ser Lys Trp Ser Lys Tyr Lys His Asp
            20   25   30

Leu Ala Ala Ser Cys Gln Gly Arg Val Val Ala Ala Glu Glu Lys Asn
        35   40   45

Gly Val Val Phe Ile Arg Gly Glu Gly Val Gly Ala Tyr Asn Pro Gln
    50   55   60

Leu Asn Leu Lys Asn Val Gln Arg Asn Leu Ile Leu Leu His Pro Gln
65   70   75   80

Leu Leu Leu Leu Val Asp Gln Ile His Leu Gly Glu Glu Ser Pro Leu
                85   90   95

Glu Thr Ala Ala Ser Phe Phe His Asn Val Asp Val Pro Phe Glu Glu
            100   105   110

Thr Val Val Asp Gly Val His Gly Ala Phe Ile Arg Gln Arg Asp Gly
        115   120   125

Leu Tyr Lys Met Tyr Trp Met Asp Asp Thr Gly Tyr Ser Glu Lys Ala
    130   135   140

Thr Phe Ala Ser Val Thr Tyr Pro Arg Gly Tyr Pro Tyr Asn Gly Thr
145   150   155   160

Asn Tyr Val Asn Val Thr Met His Leu Arg Ser Pro Ile Thr Arg Ala
                165   170   175

Ala Tyr Leu Phe Ile Gly Pro Ser Ile Asp Val Gln Ser Phe Thr Val
            180   185   190

His Gly Asp Ser Gln Gln Leu Asp Val Phe Ile Ala Thr Ser Lys His
        195   200   205

Ala Tyr Ala Thr Tyr Leu Trp Thr Gly Glu Ala Thr Gly Gln Ser Ala
    210   215   220

Phe Ala Gln Val Ile Ala Asp Arg His Lys Ile Leu Phe Asp Arg Asn
225   230   235   240

Ser Ala Ile Lys Ser Ser Ile Val Pro Glu Val Lys Asp Tyr Ala Ala
                245   250   255

Ile Val Glu Gln Asn Leu Gln His Phe Lys Pro Val Phe Gln Leu Leu
260 265 270

Glu Lys Gln Ile Leu Ser Arg Val Arg Asn Thr Ala Ser Phe Arg Lys
275 280 285

Thr Ala Glu Arg Leu Leu Arg Phe Ser Asp Lys Arg Gln Thr Glu Glu
290 295 300

Ala Ile Asp Arg Ile Phe Ala Ile Ser Gln Gln Gln Gln Gln Gln Ser
305 310 315 320

Lys Ser Lys Lys Asn Arg Arg Ala Gly Lys Arg Tyr Lys Phe Val Asp
325 330 335

Ala Val Pro Asp Ile Phe Ala Gln Ile Glu Val Asn Glu Lys Lys Ile
340 345 350

Arg Gln Lys Ala Gln Ile Leu Ala Gln Lys Glu Leu Pro Ile Asp Glu
355 360 365

Asp Glu Glu Met Lys Asp Leu Leu Asp Phe Ala Asp Val Thr Tyr Glu
370 375 380

Lys His Lys Asn Gly Gly Leu Ile Lys Gly Arg Phe Gly Gln Ala Arg
385 390 395 400

Met Val Thr Thr Thr His Ser Arg Ala Pro Ser Leu Ser Ala Ser Tyr
405 410 415

Thr Arg Leu Phe Leu Ile Leu Asn Ile Ala Ile Phe Phe Val Met Leu
420 425 430

Ala Met Gln Leu Thr Tyr Phe Gln Arg Ala Gln Ser Leu His Gly Gln
435 440 445

Arg Cys Leu Tyr Ala Val Leu Leu Ile Asp Ser Cys Ile Leu Leu Trp
450 455 460

Leu Tyr Ser Ser Cys Ser Gln Ser Gln Cys
465 470

<210> 73
<211> 3442
<212> DNA
<213> Homo sapiens

<400> 73
agcgccatag ccttaggact atcggtcaca tcctcgcgct cctgctccgg ctcctccatc 60
ttggcctcgg cagtggcggc tgccgggagg atgtgccgcc ttctggcagg gggaagaagg 120
aggagaagat gaagaagcac cggcgggcct tggccctggt ctcctgcctc tttctgtgct 180
ctctggtctg gcttcccagc tggcgtgtat gttgtaaaga gagttcttca gcttcagcgt 240
catcatatta ctctcaagat gacaactgcg cactagaaaa tgaagatgta caattccaga 300
aaaaggtgcc ttaaataaag ttaacattat aatttgtgtg tcagctttct gagagtgtct 360
gaaaacattc agaataaaag taatttcaaa aatgccatgc cataattttt ggtggagatt 420
cgtatttttc tttgctatta ctcaggtaat tcttaaatta tgacggctca gagatattta 480
tatgtttatt cttgttgctt gtagttggaa ttttgtaaca tccttagtcc tgtagtatag 540
ggtagtgcat gttcagagag ctgaaaatga gtgatttgtt tttaatgatc tataatagag 600

tttttaaaga aaccccaatt ttgcaaatga gaactattag aagtgagtat tccagggaga 660
atctacagtc agtggctttg tagtttgttt tatgtaatta ggtgcagtaa atataaagac 720
tccaaaaaac ctcatggtct taaaacatgt attattttac cattctaaat gataaatgga 780
gagtattgac ttgatttggc ttttgccttt aacttcagtg tatttattta aaattactga 840
agtaatttat attggtataa aatatttatt atttatgtct cattcctttc cccaaaggaa 900
caacagtcta ctatttcttg tgaaaacgtt tggaccttgt tctgtgggta tagataacac 960
ctttatattt gcccacaaat taatattttt atttccatga aaatatcata taaatatatt 1020
acaaattgcc atccccccttc ccctccagtg atagctcata tatcatcttt tcatgttgat 1080
atattctgaa tggctgcatt ttaatcttgt tatatagaca ttatttatca gttgttcttt 1140
attgacaaac ttttgcattt tgttccctgc catgtgtgca cacatgtggg tgtgtgtatc 1200
aacacatact tacaattaca tacttgaggg ttttttgggc atatttagag tggattattt 1260
aaatttaagt tatgttggat atatttctgg gatggagcat ttaaaatttt gaagacttgc 1320
cgcatatctc aaaaaaaact ataattttat attttcaccc acacagtata taagattttg 1380
atttaatccc ccttttgatg aagcatttg caaacaaatg tcataaaagt gaatttaagc 1440
aaagcattaa gggggaaagc atgttctttc agtaaacatt tagatacctа gtatgagcta 1500
gataggctca ggtaaacaaa gattgaatat gaactttat gaaaattaca ctctagaagg 1560
cataaaggta ttagaaattc taacttgaat gtatgtcaaa aaagagatga aagaaagagc 1620
tttatgtatc ttcatttgtc aggtattcat tggagtttta ctaggtgctt acaacggtgc 1680
tggatggtaa gactaaaatg cttattaaga aatcaaatga agttcttgaa ctggtgtatt 1740
gcacatttta aatgttgtag caatgagggg attcaaggaa atagacagta atcttgtata 1800
caaatgaaat taattagagt caaataaaca aggcagtttt ttggttttaa agtatggaaa 1860
aaaaccatct tcgtattgct ttataactgt tttgtaaaac agttttatca ggtgattttt 1920
gttgttgttg ttatatagga tgaaagagag ggacctatca atgccgaatc attgggaaaa 1980
tcaggttcaa atttacctat ttctccaaaa gaacataaat taaaagatga ttctattgtg 2040
gatgtacaag taagctatgt cgctttgatt ttcaataata tgtcatttca aactacttta 2100
caagattgaa aacctttggt caccatattg tgtgtgtatt gttagttttt tcactttgag 2160
gtactctgta actggactta agattactta cctgctaata gtactacttt tgagaacatg 2220
taaaattaca gataataata aatgtgacta gtctcttggt agtaaaagtt tgagtataaa 2280
tcctcatttc ttcctcggtt ctattttggt tcattatgat gtatcttgtc tcttcagatt 2340
ttcagttgtt aagaaatttt tttctaacct gaatcacttg gaacaaaagg gagtattttt 2400
atgtagaaca cagagtattt tgataaccag gatttccact tattgtgggt atgaatagat 2460
aatagatcaa aatatgtttt ttcccttttt ctctcatatt acattctgaa tattgtttat 2520
tttgtgcacc agactttatg aaaaatacta aaaactagaa tatatacacc ataaactgat 2580
cagaatgctg aggtatctgg aaaccatgta atatcagtaa tggctgaagg tactggggat 2640
atttttatctg taggcagaag gactaaggaa aaactaaaat ctcgaatatt aaaaaaagaa 2700
cacacatttc aactcagaat gagggagaat tctttctttt taaaaaaata cagccttggc 2760
taattttttt ttcatttttt atttttaac cttgtacttt ttgcaagagc cagggctatt 2820
ttataactta ctgagttatc taaagcaata gaattagttt cattttattg gattctggaa 2880
gacatttgtc aagggtttat gcataggagt aagagaaaaa tgatacttgt agcccttaca 2940
attgtatgac tatcctgaac actcctaccg ttattcataa aacttttatt atgatgtagt 3000
tgtgctcaaa tacttccgag tgcttaccat gtcttgtata cctatgttgt tcattacagt 3060
agccactagc cacatgtggc cattaagcac ttgaaatgcg gctagtccaa attgaaattt 3120
actgtaagtg taaaatacac attggatttt gaagacttaa ttaaaaaata gcatgtaggc 3180
cgggcacagt ggatcacctg aggtcaggag ttcgagacca gcctggccaa catggtgaaa 3240
ccctgtctct accaaaaata caaaaattag ccaggtgtgg tggtgcacgc ctatagtctc 3300
agctactcag gaggctgagg caggagaatt gcttgaaccc aggaggcgga ggttgcagtg 3360
agccgagatc atgccactgc actccagcct ggggcaacag agtgagactc tgtctcaaaa 3420
aaaaaaaaaa aaaaaaaaaa aa 3442

<210> 74
<211> 61
<212> PRT
<213> Homo sapiens

<400> 74
Met Lys Lys His Arg Arg Ala Leu Ala Leu Val Ser Cys Leu Phe Leu
1 5 10 15

Cys Ser Leu Val Trp Leu Pro Ser Trp Arg Val Cys Cys Lys Glu Ser
20 25 30

```
Ser Ser Ala Ser Ala Ser Ser Tyr Tyr Ser Gln Asp Asp Asn Cys Ala
        35                  40                  45

Leu Glu Asn Glu Asp Val Gln Phe Gln Lys Lys Val Pro
    50                  55                  60


<210> 75
<211> 1159
<212> DNA
<213> Homo sapiens

<400> 75
gagcggcggc ggtggcggcc gggagactgg gagggcttcc ggggctgccg gtctgagtgc 60
agagctgctg tcatggcggc cgctctgtgg ggcttctttc ccgtcctgct gctgctgctg 120
ctatcggggg atgtccagag ctcggaggtg cccggggctg ctgctgaggg atcgggaggg 180
agtggggtcg gcataggaga tcgcttcaag attgaggggc gtgcagttgt tccaggggtg 240
aagcctcagg actggatctc ggcggcccga gtgctggtag acggagaaga gcacgtcggt 300
ttccttaaga cagatgggag ttttgtggtt catgatatac cttctggatc ttatgtagtg 360
gaagttgtat ctccagctta cagatttgat cccgttcgag tggatatcac ttcgaaagga 420
aaaatgagag caagatatgt gaattacatc aaaacatcag aggttgtcag actgccctat 480
cctctccaaa tgaaatcttc aggtccacct tcttacttta ttaaaaggga atcgtggggc 540
tggacagact ttctaatgaa cccaatggtt atgatgatgg ttcttccttt attgatattt 600
gtgcttctgc ctaaagtggt caacacaagt gatcctgaca tgagacggga aatggagcag 660
tcaatgaata tgctgaattc caaccatgag ttgcctgatg tttctgagtt catgacaaga 720
ctcttctctt caaaatcatc tggcaaatct agcagcggca gcagtaaaac aggcaaaagt 780
ggggctggca aaggaggta gtcaggccgt ccagagctgg catttgcaca aacacggcaa 840
cactgggtgg catccaagtc ttggaaaacc gtgtgaagca actactataa acttgagtca 900
tcccgacgtt gatctcttac aactgtgtat gttaactttt tagcacatgt tttgtacttg 960
gtacacgaga aaacccagct ttcatctttt gtctgtatga ggtcaatatt gatgtcactg 1020
aattaattac agtgtcctat agaaaatgcc attaataaat tatatgaact actatacatt 1080
atgtatatta attaaaacat cttaatccag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140
aaaaaaaaaa aaaaaaaaa                                              1159

<210> 76
<211> 242
<212> PRT
<213> Homo sapiens

<400> 76
Met Ala Ala Ala Leu Trp Gly Phe Phe Pro Val Leu Leu Leu Leu Leu
1               5                   10                  15

Leu Ser Gly Asp Val Gln Ser Ser Glu Val Pro Gly Ala Ala Ala Glu
            20                  25                  30

Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Asp Arg Phe Lys Ile Glu
        35                  40                  45

Gly Arg Ala Val Val Pro Gly Val Lys Pro Gln Asp Trp Ile Ser Ala
    50                  55                  60

Ala Arg Val Leu Val Asp Gly Glu Glu His Val Gly Phe Leu Lys Thr
65                  70                  75                  80

Asp Gly Ser Phe Val Val His Asp Ile Pro Ser Gly Ser Tyr Val Val
                85                  90                  95

Glu Val Val Ser Pro Ala Tyr Arg Phe Asp Pro Val Arg Val Asp Ile
```

100 105 110

Thr Ser Lys Gly Lys Met Arg Ala Arg Tyr Val Asn Tyr Ile Lys Thr
115 120 125

Ser Glu Val Val Arg Leu Pro Tyr Pro Leu Gln Met Lys Ser Ser Gly
130 135 140

Pro Pro Ser Tyr Phe Ile Lys Arg Glu Ser Trp Gly Trp Thr Asp Phe
145 150 155 160

Leu Met Asn Pro Met Val Met Met Met Val Leu Pro Leu Leu Ile Phe
165 170 175

Val Leu Leu Pro Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg
180 185 190

Glu Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro
195 200 205

Asp Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly
210 215 220

Lys Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys
225 230 235 240

Arg Arg

<210> 77
<211> 2462
<212> DNA
<213> Homo sapiens

<400> 77
agaccggaag tgagtgatcg aaagcatggc gtcggtggtg ttggcgctga ggacccggac 60
agccgttaca tccttgctaa gcccccactcc ggctacagct cttgctgtca gatacgcatc 120
caagaagtcg ggtggtagct ccaaaaacct cggtggaaag tcatcaggca gacgccaagg 180
cattaagaaa atggaaggtc actatgttca tgctgggaac atcattgcaa cacagcgcca 240
tttccgctgg cacccaggtg cccatgtgag ttgctccgtt gctgcccccc tttttccttt 300
tctaggttga cctctccttg cccctaagca tggtaataac agttgcatgt attgagtgct 360
taccaaatgg caagcattgt gctgattccc atgcctacac gatctcattt cttccttacc 420
acatccctgt aagtaaggtg aaatgccaga gacctagacg ggtggaaggg agcaagtgac 480
tgctgggatt tgcaccaggt ctgcctaact cccagatcac tatgatttgc cctggtgttg 540
cattggcctg gtattcttgg ttctcctttc taaccctcag ttcttggagg acaagatacc 600
tggtgattta aaatattatt ttagtcttgg gaaactaatt tcaatttatt agtttttcat 660
tattctaaga cttcttcctt tgtataaact tacttgcaga tggttgaaag atagcttgaa 720
tttaatgaaa tagaattcag tgtgccagga gttaggttca taccaggtgg ggatttcagt 780
ttcagcaagt tggcatcatt tttatagggt aggacagttc tttgttacag agacataacg 840
atactgtact ctccacatta ttttaaatat tagttgcctt tgtaaacagt ttcccctccc 900
ccaccccttt ttcgataatt ttagtaggta caaaaaggtt gatagtaacc tgtatttatt 960
tcaaagatgc taatttgtat gtgaattgat tatgtatgta gtagcttttt acctttttaga 1020
acttaagaca ttagatgtgt ggctatgtca acaataataa tcaaagctaa cacattttga 1080
gctagacagt attctaggcc ctttatgatt gttgagcatt aatcctcaaa atgaccctgt 1140
aaaatagtta atattatccc catttgacag acgaaaaaat agaggcacag tgaagtaact 1200
tgcctaagac cacacaggag taagtagcag tgctggtatt tgaaccaggc atcctggctc 1260
cagagcccat tcttttaatc agagagacag agaataatgc tggactacct gggtaaaatt 1320
tgccacacac ccagcctgaa gttctaaaag aaaaagctaa aaaatatggt taaaaactgt 1380
atatacaaca cagtttaatc tctctgcttc atatttcaca tctgaaaagt ggcgttggaa 1440

ataatacctc tttcactagg tgagaattaa atgacttaat gtgtattaaa gggcttacat 1500
gggtattagc taatgcagta gtatgattgt tttattagca tatgcattat ccatatagct 1560
ttggtttata ttttccatag agcctaaact ttatagatca ctatctaaat gaaaatttac 1620
atcaaactag tgttttaata tgacagttct agtgttgttt aagtctaagt gaagatttag 1680
ggcatcttcc tgggttttgg gatttgtgca gtgtggcttc tgaccagctg catagacatg 1740
gctccaggta acagtccctg ggactgagca gtggcccatg ttggctgttg gagctttctt 1800
ttccctcatt tgttatgagt caataaagaa gcagaaggtt tggacgtgct agccagtggg 1860
aaagggaacc tgagatggag ctctctgatc accctttcag ccccagggcc cggctctgtg 1920
tgagaagtct gtcccaaaat tctgggacgg accacctcac tgaccagctg accagctgac 1980
caggtctgtg tgttgcaggt gggtgttggg aagaataaat gtctgtatgc cctggaagag 2040
gggatagtcc gctacactaa ggaggtctac gtgcctcatc ccagaaacac ggaggctgtg 2100
gatctgatca ccaggctgcc caaggtgct gtgctctaca agacttttgt ccacgtggtt 2160
cctgccaagc ctgagggcac cttcaaactg gtagctatgc tttgatgtcc tgttgaggcc 2220
atcggacaga gactggagcc caggtgacag gagatggtga taccagaagt caagggttgg 2280
ggtggcgaca cggcctcccg aggaagaggt ctgcttgatg gtgactctgc aggagactct 2340
gaagtgactg ctgggaaacc ctttgggaga cctgacctgg ggccaaaaat aaagtgagcc 2400
agcgtcatga acgcatgcta tttagggaca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2460
aa 2462

<210> 78
<211> 94
<212> PRT
<213> Homo sapiens

<400> 78
Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
1 5 10 15

Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
20 25 30

Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
35 40 45

Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
50 55 60

Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
65 70 75 80

Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
85 90

<210> 79
<211> 1178
<212> DNA
<213> Homo sapiens

<400> 79
taacttattt ttaaaggata ttttacaata atttatgata atatgcttaa agatatacta 60
ttctttcatt tttttctttt aggtttgttt tctgccctag acagtcattc aaatttgggt 120
gtcatttctt atggtgtttc catgacgact ttggaagacg tatttttaaa gctagaagtt 180
gaagcagaaa ttgaccaagc aggtaaaaac agaactaaca aaacatttta ggcaatgaat 240
cagacagatg gtgaataaga caaaaattat ataaatgtaa ttttatattt tttttagaat 300
aaagggtaga aataagtaaa taagtaatga gatacttact gatagtgata ggagtaatgc 360
aggaaataat ggggtggtct tagaaggcag cgaacttaga ttatatcatc aggaaggact 420
ttgttgagat gatacttgac ctgaggcctg tataatgaga aaaatcaagt aggtgaagat 480
tttagggcag aaattttcag ataaagaact gcaactgcaa aggtattaac tgaggaatga 540
gttggatgtc tttgagggat aaaaaaaggc taccatggcc ggagccatag tgaagctatt 600

acacagcaaa gtcaggagga tactcaaagg gatagatcat gttctgcctt tgaacgtctg 660
gaaaacaatt tcatttgttt tcctattgta gtgtggaagc tatcagagag ttttaaagca 720
aataggtacc atgatctgat ttgaattttt aaaaaaacac gttctggttg ttgaatgata 780
agagtattat aaaggaagtg tggaagtagg aagaccagtt aggaaactgc tatagttaat 840
actatcttga actagggtgt cagtgaaaat agggaggccg ggcgcagtgg ttcatgcctg 900
taatcccagc actttgggag gccaaggcag ggagatcgct tgagcccagg agttccagac 960
cagtcttggc aacatggcaa aaccttgtca caaaaaacac aaaaattagc cgggtatggt 1020
agtgtgtgcc tatagtccca actactctag aggctgcggt gggagaatca cctgaggcca 1080
ggaggtcaag gctgcagtga gccatgattg cgccactgca ctctagcctg ggcatcagaa 1140
ggagaccctg tttaaaaaaa aaaaaaaaaa aaaaaaa 1178

<210> 80
<211> 62
<212> PRT
<213> Homo sapiens

<400> 80
Met Leu Lys Asp Ile Leu Phe Phe His Phe Phe Leu Leu Gly Leu Phe
1 5 10 15

Ser Ala Leu Asp Ser His Ser Asn Leu Gly Val Ile Ser Tyr Gly Val
20 25 30

Ser Met Thr Thr Leu Glu Asp Val Phe Leu Lys Leu Glu Val Glu Ala
35 40 45

Glu Ile Asp Gln Ala Gly Lys Asn Arg Thr Asn Lys Thr Phe
50 55 60

<210> 81
<211> 1285
<212> DNA
<213> Homo sapiens

<400> 81
aaaggttcca gaaacagatg aggtagagct cacctgccag gctacaggtt atcctctggc 60
agaagtatcc tggccaaacg tcagcgttcc tgccaacacc agccactcca ggaccoctga 120
aggcctctac caggtcacca gtgttctgcg cctaaagcca cccoctggca gaaacttcag 180
ctgtgtgttc tggaatactc acgtgaggga acttactttg gccagcattg accttcaaag 240
tcagatggaa cccaggaccc atccaacttg gctgcttcac attttcatcc cctcctgcat 300
cattgctttc attttcatag ccacagtgat agccctaaga aaacaactct gtcaaaagct 360
gtattcttca aaagacacaa caaaaagacc tgtcaccaca acaaagaggg aagtgaacag 420
tgctatctga acctgtggtc ttgggagcca gggtgacctg atatgacatc taaagaagct 480
tctggactct gaacaagaat tcggtggcct gcagagcttg ccatttgcac ttttcaaatg 540
cctttggatg acccagcact ttaatctgaa acctgcaaca agactagcca acacctggcc 600
atgaaacttg ccccttcact gatctggact cacctctgga gcctatggct ttaagcaagc 660
actactgcac tttacagaat taccccactg gatcctggac ccacagaatt ccttcaggat 720
ccttcttgct gccagactga aagcaaaagg aattatttcc cctcaagttt tctaagtgat 780
ttccaaaagc agaggtgtgt ggaaatttcc agtaacagaa acagatgggt tgccaataga 840
gttatttttt atctatagct tcctctgggt actagaagag gctattgaga ctatgagctc 900
acagacaggg cttcgcacaa actcaaatca taattgacat gttttatgga ttactggaat 960
cttgatagca taatgaagtt gttctaatta acagagagca tttaaatata cactaagtgc 1020
acaaattgtg gagtaaagtc atcaagctct gtttttgagg tctaagtcac aaagcatttg 1080
ttttaacctg taatggcacc atgtttaatg gtggtttttt tttttgaact acatctttcc 1140
tttaaaaatt attggtttct ttttatttgt ttttacctta gaaatcaatt atatacagtc 1200
aaaaataaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaa 1285

<210> 82

<211> 61
<212> PRT
<213> Homo sapiens

<400> 82
```
Met Glu Pro Arg Thr His Pro Thr Trp Leu Leu His Ile Phe Ile Pro
 1               5                  10                  15

Ser Cys Ile Ile Ala Phe Ile Phe Ile Ala Thr Val Ile Ala Leu Arg
            20                  25                  30

Lys Gln Leu Cys Gln Lys Leu Tyr Ser Ser Lys Asp Thr Thr Lys Arg
        35                  40                  45

Pro Val Thr Thr Thr Lys Arg Glu Val Asn Ser Ala Ile
    50                  55                  60
```

<210> 83
<211> 654
<212> DNA
<213> Homo sapiens

<400> 83
```
gagcatagac caccaggctg agtatcctga cctgagtcat ccccagggat caggagcctc 60
cagcagggaa ccttccatta tattcttcaa gcaacttaca gctgcaccga cagttgcgat 120
gaaagttcta atctcttccc tcctcctgtt gctgccacta atgctgatgt ccatggtctc 180
tagcagcctg aatccagggg tcgccagagg ccacagggac cgaggccagg cttctaggag 240
atggctccag gaaggcggcc aagaatgtga gtgcaaagat tggttcctga gagccccgag 300
aagaaaattc atgacagtgt ctgggctgcc aaagaagcag tgcccctgtg atcatttcaa 360
gggcaatgtg aagaaaacaa gacaccaaag gcaccacaga aagccaaaca agcattccag 420
agcctgccag caatttctca aacaatgtca gctaagaagc tttgctctgc ctttgtagga 480
gctctgagcg cccactcttc caattaaaca ttctcagcca agaagacagt gagcacacct 540
accagacact cttcttctcc cacctcactc tcccactgta cccaccccta aatcattcca 600
gtgctctcaa aaagcatgtt tttcaagatc aaaaaaaaaa aaaaaaaaaa aaaa       654
```

<210> 84
<211> 119
<212> PRT
<213> Homo sapiens

<400> 84
```
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu
 1               5                  10                  15

Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His
            20                  25                  30

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln
        35                  40                  45

Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe
    50                  55                  60

Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys Pro Cys Asp His Phe
65                  70                  75                  80

Lys Gly Asn Val Lys Lys Thr Arg His Gln Arg His His Arg Lys Pro
                85                  90                  95
```

Asn Lys His Ser Arg Ala Cys Gln Gln Phe Leu Lys Gln Cys Gln Leu
100 105 110

Arg Ser Phe Ala Leu Pro Leu
115

<210> 85
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 85
aatctttttt taaataagta ttttgttgag gttgaagaat tgctggcaat taaaagaata 60
gagctaatta tggctttcat cattcattca tgtatttatt gagcacctac ttattatggt 120
gctcaacact tgttactgca agctacctta atttcccaag agtggtgcct tactctgttt 180
tttctgatat ggtcttccaa tcagtgtgtg taacatacct gttgtttatc agccattgta 240
ggtggctgtg tctgttgcat catcataaga agtttaagct ttgtgctctg ataaattgtg 300
ttctgttaaa gaggttagta ggatgaaaac agcaaaacaa taattttttc aacaaattgt 360
aaattataag aaaaagagtt ggtttgtgta caacaatttt aatgattccc ttgttcattt 420
ttgctgtgaa atgcactgaa aaaaatcctc aaaatgagtt atagttcctg tgttgggaaa 480
attgacaaat aataaaacta gagaacaaac aataatgctt ctgtctcttt tacgaatgga 540
gagagaaagt ttatattcag tagagttatt gccctgttca tttgagaggg gcatggattt 600
tctgtttaag tccttcagga atcttcagct aggtggtaaa tttaataaga gtttctaaaa 660
attgaaatgt ttaacttttta aatattctgg agatagaaga agaatataaa atgaaaccag 720
gctgatctgc atgcagtggc atttacaact aactgatcac aaccaattat agattcctta 780
ttttgtttat tgtgaggcag agtctgactc tgtcacccag gatggagtac agtgcatagc 840
tcactgcagt cttgacctcc caggctaaac caatcattcc acttcaccct cccaagtagc 900
tgagaccaca ggcacacaac accacaacca gctgattgtt gtactgtttg tatagactgg 960
atctcactat gttgcccaga ctggtcttga attcctgagc tcaagcagtc ctcccacctc 1020
agcctcccaa agtactggga ttacaggcgt gaggtacctc gcccagcccc agttacagat 1080
ttctttgttc cttctctctc ccactgctta acttgattag cctttaaaaa agaaataaat 1140
aaaaattttt aaaaaaaaaa aaaaaaaaaa aaaaaa 1176

<210> 86
<211> 78
<212> PRT
<213> Homo sapiens

<400> 86
Met Tyr Leu Leu Ser Thr Tyr Leu Leu Trp Cys Ser Thr Leu Val Thr
1 5 10 15

Ala Ser Tyr Leu Asn Phe Pro Arg Val Val Pro Tyr Ser Val Phe Ser
20 25 30

Asp Met Val Phe Gln Ser Val Cys Val Thr Tyr Leu Leu Phe Ile Ser
35 40 45

His Cys Arg Trp Leu Cys Leu Leu His His His Lys Lys Phe Lys Leu
50 55 60

Cys Ala Leu Ile Asn Cys Val Leu Leu Lys Arg Leu Val Gly
65 70 75

<210> 87
<211> 1476
<212> DNA
<213> Homo sapiens

<400> 87
gaggctgcag aggtgccatg gctgagtcac acctgctgca gtggctgctg ctgctgctgc 60
ccacgctctg tggcccaggc actgctgcct ggaccacctc atccttggcc tgtgcccagg 120
gccctgagtt ctggtgccaa agcctggagc aagcattgca gtgcagagcc ctagggcatt 180
gcctacagga agtctgggga catgtgggag ccgatgacct atgccaagag tgtgaggaca 240
tcgtccacat ccttaacaag atggccaagg aggccatttt ccaggatctc tccgagcagc 300
aattccccat tcctctcccc tattgctggc ctctgcaggg ctctgatcaa gcggatccaa 360
gccatgattc ccaagggtgc gctagctgtg gcagtggccc aggtgtgccg cgtggtacct 420
ctggtggcgg gcggcatctg ccagtgcctg gctgagcgct actccgtcat cctgctcgac 480
acgctgctgg gccgcatgct gccccagctg gtctgccgcc tcgtcctccg gtgctccatg 540
gatgacagcg ctggcccaag agaatggctg ccgcgagact ctgagtgcca cctctgcatg 600
tccgtgacca cccaggccgg gaacagcagc gagcaggcca taccacaggc aatgctccag 660
gcctgtgttg gctcctggct ggacagggaa aagtgcaagc aatttgtgga gcagcacacg 720
ccccagctgc tgaccctggt gcccaggggc tgggatgccc acaccacctg ccaggccctc 780
ggggtgtgtg ggaccatgtc cagccctctc cagtgtatcc acagccccga cctttgatga 840
gaactcagct gtccagaaaa agacaccgtc ctttaaagtg ctgcagtatg gccagacgtg 900
gtggctcaca cctgcaatcc cagcacctta ggaggccgag gcaggaggat ccttgaggtc 960
aggagttcga gaccagcctc gccaacatgg tgaaacccca tttctactaa aaatacaaaa 1020
aattagccaa gtgtggtggc atatgcctgt aatcccaact actcagaagg ccgaggcagg 1080
agaattactt gaacgcagga gaatcactgc agcccaggag gcagaggttg cagtgagccg 1140
agattgcacc actgcactcc agcctgggtg acagagcaag actccatctc agtaaataaa 1200
taaataaata aaaagcgctg cagtagctgt ggcctcaccc tgaagtcagc gggcccaggc 1260
ctacctcact ctctcccttg gcagagaagc agacgtccat agctcctctc cctcacaagc 1320
gctcccagcc tgccctccag ctgctgctct cccctcccag tctctactca ctgggatgag 1380
gttaggtcat gaggacacca aaaacctaaa aataaacaaa aagccaaaca agccttagct 1440
tttcttaaag acaaaaaaaa aaaaaaaaaa aaaaaa 1476

<210> 88
<211> 145
<212> PRT
<213> Homo sapiens

<400> 88
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Leu Ser Glu Gln Gln Phe
85 90 95

Pro Ile Pro Leu Pro Tyr Cys Trp Pro Leu Gln Gly Ser Asp Gln Ala
100 105 110

Asp Pro Ser His Asp Ser Gln Gly Cys Ala Ser Cys Gly Ser Gly Pro
115 120 125

Gly Val Pro Arg Gly Thr Ser Gly Gly Gly Arg His Leu Pro Val Pro
130 135 140

Gly
145

<210> 89
<211> 2243
<212> DNA
<213> Homo sapiens

<400> 89
agtactttgt aatcaagtga aaatataact ttattttta actctattac attttatttt 60
gtcatgtact aaaattattt ctgtattgct tttataaaaa acagtggcat ttagcactgg 120
cattgagact atagcacatc atttttgcca ttttcagtgc ttatattgtt aggtagaggc 180
tggcacttta ttagaatgca agccacaaaa atatcaattt tgtttttttt gttagggtgg 240
gtcttctttt tttctttccc tctctctttt tttaacaaat gccttcttat agaaaaactt 300
tctaagaggc aacaatttag aatggatatt ttgacgaatc ggcatgagtg taacagtgat 360
aacctgatct gtttgtttta aagattatta ccaagtgaaa aattcagaat gaatagaatt 420
tacactaaca tgctatataa aatgttaaag tctgatgctg tgaaagcaat ctagtgctat 480
atttctacct cctcatttgt cttaattatt tggtaagtgg gattatgatg agtaactgga 540
ggggcttaga aacaaaaact ggatgaaaga gtatgcatga agaaaagctt ctttgataaa 600
tgtggagttc ttcattataa atatatattc atgaattcac agataagtac ttaagaaaca 660
gacagtttac ttggcctaaa aatattttga tgtttactca aaaagtacct cttcaggtct 720
tgagaacatg gaaaagaatt gagtgctttt aaatactttt tagaaagtaa tcataaaagt 780
aaattgaatt tcaaacctat ttggcttctg ttttgtgaac ctttgaacta tatgtatgtg 840
tataagggta tacacataca tatatggcat ataacaagtg tacacatata cacataacaa 900
gtgtagaagt atatattaca tacatacact cactctgtct ggtataggct aattttgaag 960
aactcccata agtttctgct gcttctccca taactgctgc caccaccatc agaattcata 1020
atcaaaccta accttttgt ttggggcacc aaatctgaag acaaaattaa tttgcaccag 1080
taaacttcaa gctgctttct ttcttgaaaa ctaaacgttt aacgtataat gtctgtttgg 1140
atactgttcc aaattgttga ttgcatgtgg ttaatgttgc attagagcac tttgcaattg 1200
cataattcat taatgttttg tgagcttgca tttgtgagtt attggatgat cagactgaat 1260
tttgtcaagt atcacattgt acatcttgcc tagatgtcga tgactgcaag taataataca 1320
gtttataatg aaactatcta caattcttgt tttagcacat ctgttatccg taaaacacct 1380
gtaactagct tttttaattt attatttgaa ttttaggata gcgaatcact aatttttagt 1440
tgctgaggtt ggcattttag tgattattaa gcacttctgt cagtctttga aaaaagaacg 1500
tattttttgt gctttgaaga tctctgaaga atttctttta taatagaatg ggcatgtatt 1560
gtaacagttt tatgtcaaat gatctgtgct gtagaaaaac attaaccctt gttcaaaaaa 1620
gaaatggata aacttggcct ttctaagtgg taagaatgac ctgtcactat aatatactgt 1680
atgtttacat tttatttaaa ttttatctct tatgtatagg gtgataacct tccccagaaa 1740
caacagtgat tgcgattgtt ttctagaaac ttctttaaag tgccacattt ggcagtacaa 1800
atgagtctga gtgtaatagc ccagagattt atatatagtt gaatgtctaa aatggtaaaa 1860
tgtgccactg tgtcaagtta cagtggctta tgtttttcat agtaattcaa atgaacttcc 1920
tatttttgat agtaaatgtc atttaatagt atacttgcca tttgagcctc actgcaaaat 1980
tagtgcagag gagaaaacaa tttttaatgt aatcttgatt ttacctcata tactgtacat 2040
tccaaaaact ctaaactttt taaagattat agatacacta ccaaacatat caccttaaaa 2100
ttgtataagg ctgaatgaac ttcatacaaa tgaaaaaaat ctcataaaaa tacataaact 2160
atgtagcaaa agtatctgta aaatccatgg aaaataaaag ttgtatcatt ctttttgaaa 2220
aaaaaaaaaa aaaaaaaaaa aaa 2243

<210> 90
<211> 61
<212> PRT
<213> Homo sapiens

<400> 90
Met Gln Ala Thr Lys Ile Ser Ile Leu Phe Phe Leu Leu Gly Trp Val
1 5 10 15

Phe Phe Phe Ser Phe Pro Leu Ser Phe Phe Asn Lys Cys Leu Leu Ile

20 25 30

Glu Lys Leu Ser Lys Arg Gln Gln Phe Arg Met Asp Ile Leu Thr Asn
35 40 45

Arg His Glu Cys Asn Ser Asp Asn Leu Ile Cys Leu Phe
50 55 60

<210> 91
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 91
aaatgggctg tcttcatcgg tggaatacaa cataatggag ttggaacaag aacttgaaaa 60
tgtaaagact cttaagacaa aattagagag gcgaaaaaag gcttcagcat gggaaagaaa 120
tttggtgtat cccgctgtta tggttctcct tcttattgag acatccatct cggtcctctt 180
ggtggcttgt aatattcttt gcctattggt tgatgaaaca gcaatgccaa aggaacaag 240
ggggcctgga ataggaaatg cctctctttc tacgtttggt tttgtgggag ctgcgcttga 300
aatcattttg attttctatc ttatggtgtc ctctgttgtc ggcttctata gccttcgatt 360
ttttggaaac tttactccca agaaagatga cacaactatg acaaagatca ttggaaattg 420
tgtgtccatc ttggttttga gctctgctct gcctgtgatg tcgagaacac tgggaatcac 480
tagatttgat ctacttggcg actttggaag gtttaattgg ctgggaaatt tctatattgt 540
attatcctac aatttgcttt ttgctattgt gacaacattg tgtctggtcc gaaaattcac 600
ctctgcagtt cgagaagaac ttttcaaggc cctagggctt cataaacttc acttaccaaa 660
tacttcaagg gattcagaaa cagccaagcc ttctgtaaat gggcatcaga aagcactgtg 720
agacgcacag acggcgtctt ctgccaccaa gagacccgag aactccagat tcacgacatt 780
cctgtcccat gtagaagcat ttccattcaa ccgtggcccc tcttcagaac ctagacctat 840
cagtgccatt tttttttcat aatctacgaa gaacttggct atggctgatc tttttaaat 900
ttaactttct gatggaccct gtagtttcca gttaagtgca gattccttac agacatatag 960
aacagcgcat tcttctgtag acatttgctc atgttggtaa atacaatcac ccatatgaaa 1020
aaaaaaaaaa aaaaaaaaaa a 1041

<210> 92
<211> 228
<212> PRT
<213> Homo sapiens

<400> 92
Met Glu Leu Glu Gln Glu Leu Glu Asn Val Lys Thr Leu Lys Thr Lys
1 5 10 15

Leu Glu Arg Arg Lys Lys Ala Ser Ala Trp Glu Arg Asn Leu Val Tyr
20 25 30

Pro Ala Val Met Val Leu Leu Leu Ile Glu Thr Ser Ile Ser Val Leu
35 40 45

Leu Val Ala Cys Asn Ile Leu Cys Leu Leu Val Asp Glu Thr Ala Met
50 55 60

Pro Lys Gly Thr Arg Gly Pro Gly Ile Gly Asn Ala Ser Leu Ser Thr
65 70 75 80

Phe Gly Phe Val Gly Ala Ala Leu Glu Ile Ile Leu Ile Phe Tyr Leu
85 90 95

Met Val Ser Ser Val Val Gly Phe Tyr Ser Leu Arg Phe Phe Gly Asn
100 105 110

```
Phe Thr Pro Lys Lys Asp Asp Thr Thr Met Thr Lys Ile Ile Gly Asn
        115                 120                 125

Cys Val Ser Ile Leu Val Leu Ser Ser Ala Leu Pro Val Met Ser Arg
    130                 135                 140

Thr Leu Gly Ile Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe
145                 150                 155                 160

Asn Trp Leu Gly Asn Phe Tyr Ile Val Leu Ser Tyr Asn Leu Leu Phe
                165                 170                 175

Ala Ile Val Thr Thr Leu Cys Leu Val Arg Lys Phe Thr Ser Ala Val
            180                 185                 190

Arg Glu Glu Leu Phe Lys Ala Leu Gly Leu His Lys Leu His Leu Pro
        195                 200                 205

Asn Thr Ser Arg Asp Ser Glu Thr Ala Lys Pro Ser Val Asn Gly His
    210                 215                 220

Gln Lys Ala Leu
225


<210> 93
<211> 1792
<212> DNA
<213> Homo sapiens

<400> 93
atgggacggg acttgcggcc cgggtcccgc gtgctcctgc tcctgcttct gctcctgctg 60
gtgtacctga ctcagccagg caatggcaac gagggcagcg tcactggaag ttgttattgt 120
ggtaaaagaa tttcttccga ctccccgcca tcggttcagt tcatgaatcg tctccggaaa 180
cacctgagag cttaccatcg gtgtctatac tacacgaggt tccagctcct ttcctggagc 240
gtgtgtggag gcaacaagga cccatgggtt caggaattga tgagctgtct tgatctcaaa 300
gaatgtggac atgcttactc ggggattgtg gcccaccaga agcatttact tcctaccagc 360
cccccaactt ctcaggcctc agagggggca tcttcagata tccacacccc tgcccagatg 420
ctcctgtcca ccttgcagtc cactcagcgc cccaccctcc cagtaggatc actgtcctcg 480
gacaaagagc tcactcgtcc caatgaaacc accattcaca ctgcgggcca cagtctggca 540
gttgggcctg aggctgggga gaaccagaag cagccggaaa aaaatgctgg tcccacagcc 600
aggacatcag ccacagtgcc ggtcctgtgc ctcctggcca tcatcttcat cctcaccgca 660
gccctttcct atgtgctgtg caagaggagg agggggcagt caccgcagtc ctctccagat 720
ctgccggttc attatatacc tgtggcacct gactctaata cctgagccaa gaatggaagt 780
ttgtgaggag acggactcta tgttgcccag gctgttatgg aactcctgag tcaagtgatc 840
ctcccacctt ggcctctgaa ggtgcgagga ttataggcgt cacctaccac atccagccta 900
cacgtatttg ttaatatcta acataggact aaccagccac tgccctctct taggcccctc 960
atttaaaaac ggttatacta taaaatctgc ttttcacact gggtgataat aacttggaca 1020
aattctatgt gtattttgtt ttgttttgct ttgctttgtt ttgagacgga gtctcgctct 1080
gtcatccagg ctggagtgca gtggcatgat ctcggctcac tgcaaccccc atctcccagg 1140
ttcaagcgat tctcctgcct cctcctaagt agctgggact acaggtgctc accaccacac 1200
ccggctaatt ttttgtattt ttagtagaga cggggtttca ccatgttgac caggctggtc 1260
tcgaactcct gacctggtga tctgcccacc caggcctccc aaagtgctgg gattaaaggt 1320
gtgagccacc atgcctggcc ctatgtgtgt tttttaacta ctaaaaatta tttttgtaat 1380
gattgagtct tctttatgga aacaactggc ctcagccctt gcgcccttac tgtgattcct 1440
ggcttcattt tttgctgatg gttccccctc gtcccaaatc tctctcccag tacaccagtt 1500
gttcctcccc cacctcagcc ctctcctgca tcctcctgta cccgcaacga aggcctgggc 1560
tttcccaccc tccctcttag caggtgccgt gctgggacac catacgggtt ggtttcacct 1620
cctcagtccc ttgcctaccc cagtgagagt ctgatcttgt ttttattgtt attgctttta 1680
```

ttattattgc ttttattatc attaaaactc tagttcttgt tttgtctctc cgaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1792

<210> 94
<211> 254
<212> PRT
<213> Homo sapiens

<400> 94
Met Gly Arg Asp Leu Arg Pro Gly Ser Arg Val Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Val Tyr Leu Thr Gln Pro Gly Asn Gly Asn Glu Gly
20 25 30

Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser Ser Asp Ser
35 40 45

Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His Leu Arg Ala
50 55 60

Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu Ser Trp Ser
65 70 75 80

Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys
85 90 95

Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile Val Ala His
100 105 110

Gln Lys His Leu Leu Pro Thr Ser Pro Pro Thr Ser Gln Ala Ser Glu
115 120 125

Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr
130 135 140

Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser
145 150 155 160

Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His Thr Ala Gly
165 170 175

His Ser Leu Ala Val Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro
180 185 190

Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val
195 200 205

Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Leu Ser Tyr
210 215 220

Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp
225 230 235 240

Leu Pro Val His Tyr Ile Pro Val Ala Pro Asp Ser Asn Thr
245 250

<210> 95
<211> 1234

<212> DNA
<213> Homo sapiens

<400> 95
gagactccag atttccctgt caaccacgag gagtccagag aggaaacgcg gagcggagac 60
aacagtacct gacgcctctt tcagcccggg atcgccccag cagggatggg cgacaagatc 120
tggctgccct tccccgtgct ccttctggcc gctctgcctc cggtgctgct gcctggggcg 180
gccggcttca caccttccct cgatagcgac ttcaccttta cccttcccgc cggccagaag 240
gagtgcttct accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa aaccttagtt 360
tttgaacaaa gaaaatcaga tggagttcac actgtagaga ctgaagttgg tgattacatg 420
ttctgctttg acaatacatt cagcaccatt tctgagaagg tgattttctt tgaattaatc 480
ctggataata tgggagaaca ggcacaagaa caagaagatt ggaagaaata tattactggc 540
acagatatat tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc tcgtgatcga 660
aacatacaag aaagcaactt tgatagagtc aatttctggt ctatggttaa tttagtggtc 720
atggtggtgg tgtcagccat tcaagtttat atgctgaaga gtctgtttga agataagagg 780
aaaagtagaa cttaaactc caaactagag tacgtaacat tgaaaaatga ggcataaaaa 840
tgcaataaac tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc tgtgcaagta 960
atcctgctga tccagttgta cttaagtgtg taacaggaat attttgcaga atataggttt 1020
aactgaatga agccatatta ataactgcat tttcctaact ttgaaaaatt ttgcaaatgt 1080
cttaggtgat ttaaataaat gagtattggg cctaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

<210> 96
<211> 229
<212> PRT
<213> Homo sapiens

<400> 96
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
1 5 10 15

Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
20 25 30

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
35 40 45

Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
50 55 60

Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
65 70 75 80

Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
85 90 95

Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
100 105 110

Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
115 120 125

Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
130 135 140

Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile

145 150 155 160

Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
165 170 175

Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
180 185 190

Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
195 200 205

Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
210 215 220

Arg Lys Ser Arg Thr
225

<210> 97
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 97
gtgcttcctg gcaggagagc agatgtgatt ctgagcgaca tggcgcccaa tgccacaggg 60
ttccgggacc tcgatcatga caggctcatc agcctgtgcc tgacccttct cagcgtgacc 120
ccagacatcc tgcaacctgg ggggacattc ctttgtaaaa cctgggctgg aagtcaaagc 180
cgtcggttac agaggagact gacagaggaa ttccagaatg taaggatcat caaacctgaa 240
gccagcagga aagagtcatc agaagtgtac ttcttggcca cacagtacca cggaaggaag 300
ggcactgtga agcagtgagg atttcttgtg ccattttcat aatggtcatt agctcctttt 360
aagctagaaa cgtagcctga gctcctgaag agttcctggg agatttgagc tgattttgga 420
gatggagcag gacaagtggg gagtctctct ctctctttct ctctctctct ttttaaccaa 480
aaagagatga caaaactaag ttcaggggcc atggaaaatg aaaaagtccg ctatattgtg 540
atttgggaag agaaagttat caagagaaag aggtgaggat ggaaggatgg agaaaaacag 600
actgtgggaa ggatcagaag gaatccgccg aggcagggat gggtgtgccc atgtgtgcct 660
tgacgggact tcatcttata gactgttaaa ctgtcacaca caaacaggct ttccacccct 720
gctctgagag caccacgcac agatttccag ttcttagtgt ggctgtttaa agtagaaaat 780
ctgggggctg ggtgaggcca ctcatgcctg taaacccagg gctttagaag gctgaggctg 840
ggggattgct tgaagtcagg agttcaagac caacctgggc aacatagcaa caccccccat 900
gtctacaaaa atgaaaaacc aaaaagcaaa ccaaaagaaa aatctgaaat ttccatctgg 960
ggattaactt ctgtctttct ggtgaacaat atagcaattc acgcattctt caagcagcaa 1020
aagttcccgg aacaattagg gaagacgtat ggtctgaatt tatccaggca gtgggtctgc 1080
tttggttttt gctggaaatt tatatcagtg tctgggctcc caagaacata aatgtaattg 1140
ccaaagcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 98
<211> 92
<212> PRT
<213> Homo sapiens

<400> 98
Met Ala Pro Asn Ala Thr Gly Phe Arg Asp Leu Asp His Asp Arg Leu
1 5 10 15

Ile Ser Leu Cys Leu Thr Leu Leu Ser Val Thr Pro Asp Ile Leu Gln
20 25 30

Pro Gly Gly Thr Phe Leu Cys Lys Thr Trp Ala Gly Ser Gln Ser Arg
35 40 45

Arg Leu Gln Arg Arg Leu Thr Glu Glu Phe Gln Asn Val Arg Ile Ile
50 55 60

Lys Pro Glu Ala Ser Arg Lys Glu Ser Ser Glu Val Tyr Phe Leu Ala
65 70 75 80

Thr Gln Tyr His Gly Arg Lys Gly Thr Val Lys Gln
85 90

<210> 99
<211> 1343
<212> DNA
<213> Homo sapiens

<400> 99
```
tttttttttt tttttttttt ttttttgaga cggagtctcg ctctgttgcc caggctggag 60
tgcagtggca tgatctcgac tcactgcaat ctatgcctcc caggttcaag cgattctcct 120
gccctaggct cccgcatagc tgggattaca ggcaagcacc accacctctg gctgattttt 180
atatttttag tagagacggg gtttcaccat gttggccacg ctagcatctc aagcttcttg 240
ataaccgaca agtcaaggcc aaagatttca ggcaccagat accaccaagt gcgtttacca 300
acatttgtat gttttccttt atttatgtcc tgctttttgg catggaaatt gacctctaaa 360
ctgtacaact cagatcttaa gacagggaaa tacagtgaac actccatatc cacgggttcc 420
acatttgtgg attcaaccaa ctacagattg aaaatatttg gaaaaataaa aaggatagtt 480
gtgtttgtac tgaacatgaa cagatttctt ttttgtcatc atttcctaaa caatacaaca 540
gcgatgtaca cacagtacct tagctcattc accaaaatta cctgtgcatc cagagcccca 600
ttttcctacc aatcacatct gcatgtggtg gtgcttttcc agttagaaaa caaaactggt 660
gtcctgtgtg ctgtcaacca aacaaaactt ttcatgcagt aagcgttgtt ccattttatg 720
tggccgacag agttgtgtta acaaagtatt tggtcagcgt agaaaatctc aagggctcta 780
gaatttacag tggaactttg aagtactgta tcttgaactt gtaaaaagga gggggaacct 840
caactgtact caggaaatag aatctcaagt gagtttataa aaagctgtga tctcggtgga 900
ctttctgggc cagcagacag tgggagcagc ccaggggctc tagggagagc cccctgctga 960
gtgtccctgg cccccatggg aaactttcca ttaaaggcct ggtggatggg gtgggggtag 1020
tggggatgct aaagacgcat ttcctgagct tgtttctggt tgatacattg atgactcaga 1080
caagcgtctt cttactcatc tagttcgagc tgctagggaa gaaagcattc aagacctgat 1140
acttatctga ggagtggcag gaagtctggg gtgacttttc tcaaggtggg gggacaaaga 1200
gaatgagagg aaaatgaaac agagtgtaaa ccaaaaataa aattccaagt ccgcctacca 1260
tcggaatgga cccctcctct cagccgaggg cattccaaag tcaacctatg aaactacttc 1320
aggccatgag aggaagggga gga                                          1343
```

<210> 100
<211> 210
<212> PRT
<213> Homo sapiens

<400> 100
Met Ile Ser Thr His Cys Asn Leu Cys Leu Pro Gly Ser Ser Asp Ser
1 5 10 15

Pro Ala Leu Gly Ser Arg Ile Ala Gly Ile Thr Gly Lys His His His
20 25 30

Leu Trp Leu Ile Phe Ile Phe Leu Val Glu Thr Gly Phe His His Val
35 40 45

Gly His Ala Ser Ile Ser Ser Phe Leu Ile Thr Asp Lys Ser Arg Pro
50 55 60

Lys Ile Ser Gly Thr Arg Tyr His Gln Val Arg Leu Pro Thr Phe Val

65 70 75 80

Cys Phe Pro Leu Phe Met Ser Cys Phe Leu Ala Trp Lys Leu Thr Ser
85 90 95

Lys Leu Tyr Asn Ser Asp Leu Lys Thr Gly Lys Tyr Ser Glu His Ser
100 105 110

Ile Ser Thr Gly Ser Thr Phe Val Asp Ser Thr Asn Tyr Arg Leu Lys
115 120 125

Ile Phe Gly Lys Ile Lys Arg Ile Val Val Phe Val Leu Asn Met Asn
130 135 140

Arg Phe Leu Phe Cys His His Phe Leu Asn Asn Thr Thr Ala Met Tyr
145 150 155 160

Thr Gln Tyr Leu Ser Ser Phe Thr Lys Ile Thr Cys Ala Ser Arg Ala
165 170 175

Pro Phe Ser Tyr Gln Ser His Leu His Val Val Val Leu Phe Gln Leu
180 185 190

Glu Asn Lys Thr Gly Val Leu Cys Ala Val Asn Gln Thr Lys Leu Phe
195 200 205

Met Gln
210

<210> 101
<211> 1529
<212> DNA
<213> Homo sapiens

<400> 101
gcccggggcc cccacgtcct ttgagccgcg gaggccccct cccctgcgcc ccggcgtgac 60
ctcagccccc ggcttccccc atctgcccac agccaacccc acagggcctg gggagcgggg 120
cccgccgggc gcagtggagg tgatccggga gtccagcagc accacgggca tggtggtggg 180
cattgtggcg gcggcggcgc tctgcatcct catcctcctc tacgccatgt ataagtaccg 240
caatcgtgat gagggctcct accaggtgga ccagagccga aactacatca gtaactcggc 300
ccagagcaat ggggcggtgg tgaaagagaa ggccccggct gcccccaaga cgcccagcaa 360
ggccaagaag aacaaagaca aggagtatta tgtctgagcc cccggcactg cgcccccactg 420
ccagctgccc ctcctgggag ggcccgggag gagggtgcca ccctctccct gccaggggcc 480
tggggaccct ctccctggct gcctcaggct tctcttacga agaggaaacg caaaaaaaga 540
aaaggaaaaa ccccgtgctc gccccccttcc tcctgccgtc cactgcgcgg cctcgtcagt 600
cccggggctg actgtccctc tcagctctgc gcctgccagg cagggcacgt gctcacagcc 660
ctgggttgat ttattttttt aaggggggtag ttttattttg gtggggttgg gtgggaagga 720
aggctggggg ttttgtaaag tgtccactgc tcgtcctgtt aattttcctc aatttttctt 780
cttcttcctt ctgtccctcc tgccttcctt ctcttcccaa gccttccaat ccccatccca 840
ggcttgctgt gtctcactgt ccccaccctc cttccctact tcttttttttg tgtgtctggt 900
ttctcccttc ctttcctccc tttgggtttc cagagtcggt gggagaaggg cgggagggtg 960
ggcccgagtg gcccagtggg tgggtggggt ggggtggggc aagtgcccca actcccctca 1020
ccaggagagg cacctgcttg gtgccgccca gggaagggc tcaggcctga cggaaggcct 1080
gttctgtgtg tgccgccggg cgacgtgcat tgatggggaa gctgctggag gagcaggggt 1140
ggggggtggg agggagggga aaggcaaatg cagatatata ttacagacaa atactctaga 1200
ttccacgagc agcagcctgt ggcacccgct gggcgcgggc agcagggaag agggagcaag 1260
gcattgtcca cagactgctg gggtcacttc tttgcccacg ggctccctgc tcccccagtt 1320
ttttttctct ctttgttaac aaatgtgtct gagtcttgga aaacacccca accccggaaa 1380
tgtgtgggaa aaagaaaaca aaaactttcc aaattccaaa aaaaaaaaaa aaaaaaaaaa 1440

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1529

<210> 102
<211> 75
<212> PRT
<213> Homo sapiens

<400> 102
Met Val Val Gly Ile Val Ala Ala Ala Ala Leu Cys Ile Leu Ile Leu
1 5 10 15

Leu Tyr Ala Met Tyr Lys Tyr Arg Asn Arg Asp Glu Gly Ser Tyr Gln
20 25 30

Val Asp Gln Ser Arg Asn Tyr Ile Ser Asn Ser Ala Gln Ser Asn Gly
35 40 45

Ala Val Val Lys Glu Lys Ala Pro Ala Ala Pro Lys Thr Pro Ser Lys
50 55 60

Ala Lys Lys Asn Lys Asp Lys Glu Tyr Tyr Val
65 70 75

<210> 103
<211> 733
<212> DNA
<213> Homo sapiens

<400> 103
ttgtgtcacc attcttgttg ctttttaaaa atcaggctaa tcatgtggtc catgtctctt 60
caaagcttga cctgcacaaa tgccatattt ctatttggac cacatattct ccattttgca 120
ttgagcagta gagtacagtg gaaagggaat aagaatactg attattctga acagtttagt 180
cccaagagaa tagcgtttta aaaaagaaaa acaagatttg gagtcattgt gggttatttt 240
tggtgggatg gaggatctta aaaatgccta attgtgagag aatcaattgc tgaaagtgtt 300
aaaatttctg aaaataaatg cttaattaca tatacaggaa ttaaatagtt tggaagaggg 360
ttggattatc attaccttta caatactgta taatcagaag ttctctgaac ctcaattgta 420
tatctagaca taaaaattgt tttctgtata ggatgttgtt tggtttgttt ctgagtgttt 480
aaattttgca aaaacaaatg ttaaatttgt gcttcagtac ctagataaat tggaaaggtt 540
aatgttctag tttctggaag gtaagcctgg gagacacata agcaattcac tgctataatt 600
tagttgatgt aaaatgacgg aaactgactc aatatgtcag gtttaactct gcccaaaagc 660
agcagacatg taagcagatg tgcaataaaa aatgatcttg atccatttca aaaaaaaaaa 720
aaaaaaaaaa aaa 733

<210> 104
<211> 52
<212> PRT
<213> Homo sapiens

<400> 104
Met Trp Ser Met Ser Leu Gln Ser Leu Thr Cys Thr Asn Ala Ile Phe
1 5 10 15

Leu Phe Gly Pro His Ile Leu His Phe Ala Leu Ser Ser Arg Val Gln
20 25 30

Trp Lys Gly Asn Lys Asn Thr Asp Tyr Ser Glu Gln Phe Ser Pro Lys
35 40 45

Arg Ile Ala Phe
50

<210> 105
<211> 2342
<212> DNA
<213> Homo sapiens

<400> 105
gaaccacaaa acccgccagg ccggtgcggg agctgcggag catccgctgc ggtcctcgcc 60
gagaccccccg cgcggattcg ccggtccttc ccgcgggcgc gacagagctg tcctcgcacc 120
tggatggcag caggggcgcc ggggtcctct cgacgccaga gagaaatctc atcatctgtg 180
cagccttctt aaagcaaact aagaccagag ggaggattat ccttgacctt tgaagaccaa 240
aactaaactg aaatttaaaa tgttcttcgg gggagaaggg agcttgactt acactttggt 300
aataatttgc ttcctgacac taaggctgtc tgctagtcag aattgcctca aaaagagtct 360
agaagatgtt gtcattgaca tccagtcatc tctttctaag ggaatcagag gcaatgagcc 420
cgtatatact tcaactcaag aagactgcat taattcttgc tgttcaacaa aaaacatatc 480
aggggacaaa gcatgtaact tgatgatctt cgacactcga aaaacagcta gacaacccaa 540
ctgctaccta tttttctgtc ccaacgagga agcctgtcca ttgaaaccag caaaaggact 600
tatgagttac aggataatta cagattttcc atctttgacc agaaatttgc caagccaaga 660
gttaccccag gaagattctc tcttacatgg ccaattttca caagcagtca ctcccctagc 720
ccatcatcac acagattatt caaagcccac cgatatctca tggagagaca cactttctca 780
gaagtttgga tcctcagatc acctggagaa actatttaag atggatgaag caagtgccca 840
gctccttgct tataaggaaa aaggccattc tcagagttca caattttcct ctgatcaaga 900
aatagctcat ctgctgcctg aaaatgtgag tgcgctccca gctacggtgg cagttgcttc 960
tccacatacc acctcggcta ctccaaagcc cgccaccctt ctacccacca atgcttcagt 1020
gacaccttct gggacttccc agccacagct ggccaccaca gctccacctg taaccactgt 1080
cacttctcag cctcccacga ccctcatttc tacagttttt acacgggctg cggctacact 1140
ccaagcaatg gctacaacag cagttctgac taccaccttt caggcaccta cggactcgaa 1200
aggcagctta gaaaccatac cgtttacaga aatctccaac ttaactttga acacagggaa 1260
tgtgtataac cctactgcac tttctatgtc aaatgtggag tcttccacta tgaataaaac 1320
tgcttcctgg gaaggtaggg aggccagtcc aggcagttcc tcccagggca gtgttccaga 1380
aaatcagtac ggccttccat ttgaaaaatg gcttcttatc gggtccctgc tctttggtgt 1440
cctgttcctg gtgataggcc tcgtcctcct gggtagaatc ctctcggaat cactccgcag 1500
gaaacgttac tcaagactgg attatttgat caatgggatc tatgtggaca tctaaggatg 1560
gaactcggtg tctcttaatt catttagtaa ccagaagccc aaatgcaatg agtttctgct 1620
gacttgctag tcttagcagg aggttgtatt ttgaagacag gaaaatgccc ccttctgctt 1680
tcctttttttt tttttggaga cagagtcttg ctctgttgcc caggctggag tgcagtagca 1740
cgatctcggc tctcaccgca acctccgtct cctgggttca agcgattctc ctgcctcagc 1800
ctcctaagta tctgggatta caggcatgtg ccaccacacc tgggtgattt ttgtattttt 1860
agtagagacg gggtttcacc atgttggtca ggctggtctc aaactcctga cctagtgatc 1920
cacccctcctc ggcctcccaa agtgctggga ttacaggcat gagccaccac agctggcccc 1980
cttctgtttt atgtttggtt tttgagaagg aatgaagtgg gaaccaaatt aggtaatttt 2040
gggtaatctg tctctaaaat attagctaaa aacaaagctc tatgtaaagt aataaagtat 2100
aattgccata taaatttcaa aattcaactg gcttttatgc aaagaaacag gttaggacat 2160
ctaggttcca attcattcac attcttggtt ccagataaaa tcaactgttt atatcaattt 2220
ctaatggatt tgcttttctt tttatatgga ttcctttaaa acttattcca gatgtagttc 2280
cttccaatta aatatttgaa taaatctttt gttactcaaa aaaaaaaaaa aaaaaaaaaa 2340
aa 2342

<210> 106
<211> 431
<212> PRT
<213> Homo sapiens

<400> 106
Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile Ile
1 5 10 15

```
Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu Lys Lys
            20                  25                  30

Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu Ser Lys Gly
        35                  40                  45

Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln Glu Asp Cys Ile
    50                  55                  60

Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly Asp Lys Ala Cys Asn
65                  70                  75                  80

Leu Met Ile Phe Asp Thr Arg Lys Thr Ala Arg Gln Pro Asn Cys Tyr
                85                  90                  95

Leu Phe Phe Cys Pro Asn Glu Glu Ala Cys Pro Leu Lys Pro Ala Lys
            100                 105                 110

Gly Leu Met Ser Tyr Arg Ile Ile Thr Asp Phe Pro Ser Leu Thr Arg
        115                 120                 125

Asn Leu Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His Gly
    130                 135                 140

Gln Phe Ser Gln Ala Val Thr Pro Leu Ala His His His Thr Asp Tyr
145                 150                 155                 160

Ser Lys Pro Thr Asp Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe
                165                 170                 175

Gly Ser Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser
            180                 185                 190

Ala Gln Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln
        195                 200                 205

Phe Ser Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser
    210                 215                 220

Ala Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
225                 230                 235                 240

Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr Pro
                245                 250                 255

Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val Thr
            260                 265                 270

Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe Thr
        275                 280                 285

Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr Ala Val Leu Thr
    290                 295                 300

Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly Ser Leu Glu Thr Ile
305                 310                 315                 320

Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu Asn Thr Gly Asn Val Tyr
                325                 330                 335
```

Asn Pro Thr Ala Leu Ser Met Ser Asn Val Glu Ser Ser Thr Met Asn
340 345 350

Lys Thr Ala Ser Trp Glu Gly Arg Glu Ala Ser Pro Gly Ser Ser Ser
355 360 365

Gln Gly Ser Val Pro Glu Asn Gln Tyr Gly Leu Pro Phe Glu Lys Trp
370 375 380

Leu Leu Ile Gly Ser Leu Leu Phe Gly Val Leu Phe Leu Val Ile Gly
385 390 395 400

Leu Val Leu Leu Gly Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg
405 410 415

Tyr Ser Arg Leu Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
420 425 430

<210> 107
<211> 3153
<212> DNA
<213> Homo sapiens

<400> 107
agcgccttgc caaaatggag cttgtaagaa ggctcatgcc attgaccctc ttaattctct 60
cctgtttggc ggagctgaca atggcggagg ctgaaggcaa tgcaagctgc acagtcagtc 120
tagggggtgc caatatggca gagacccaca aagccatgat cctgcaactc aatcccagtg 180
agaactgcac ctggacaata gaaagaccag aaaacaaagc atcagaatta tcttttccta 240
tgtccagctt gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac 300
ctccagcaat gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttcctgtatt 360
tgaatcatca tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag 420
aactgtcttt gtcttctact acttcttctc tcctaacatc tgtaagtcct catttacaca 480
accttcaccc acatctccta caagcacagg ttacacactc ttctgtccgg gttcttataa 540
tcttcagtct gagtatattc cctcagagtc ttctctatct gagagagcag tagttctcta 600
acttacatgt gcataagaat catctggaga gcttgttaaa tcacagatcc tggaccccat 660
cacagatatt gtgattcatt ggttctggat ggagcacatg atcttgactt tctaactagc 720
tcccagatga ggcagagaca aggggctgat cagatggcta catattgagg ggtactgtgt 780
tagagcccaa agcggagatt ctgcattcag cctgtttaat agtaaccctg gtatcttctg 840
caatgcctct tcagggactg cacctcccta tgctctgatt ccttagatct tggttcgggt 900
tgttgaacct tcctgtttaa caagtccccc ggatgattct gacaaagaag actggagagt 960
gcatgctggg aatctctggg ctcaccattg aaatttaaga ctgtcaggtg attggaggct 1020
acatttacag ggctctgcat tcacagcacc tacattccac tgtgatccga agcagaatgc 1080
caagaacatc tgcgagtggg ttcatgagga gagctccact gtggatttct ttccaaggcc 1140
cagagctgac catgtcactc tcctgctaaa accactgact tcttggtacc agcagatctc 1200
cagagtgcag cagtcaaggt tttcccacgc tggacccagg ccaccttttc aagccttgcc 1260
tctagctgct gcctggcgtg caccctatgc ttcagccaat ctaaaccatt ttacagctcc 1320
aaaaagagct ctctgcattg tttctccaca tttcatctgt ccagctgctt ccttatgtac 1380
ttactgggga aaggagagac caagggctgc ttcatgaagt agtggcggat gagactggaa 1440
agctgagctg gtgagagtga ggaagagcct tcaagggagg gtgtgacttt attttctatg 1500
gcgcaattca ggtaatggga gtctctccag atgcaacaca tgttacagca caactttaat 1560
atgattcgtt tggcaatagt ataaagattc cctctctgcc ctgcaccagt ggacagaaat 1620
ttcaatgata aaaaaggatg aaaacctcaa tatgtgaccc atgggaaaga tagagatgga 1680
atcatactca ggagagatgt gttaagctca atgcacaaca cagaaattaa aagcagtctc 1740
tattttgatg ttcattcttg accaccttca catccatttc agctattcca aactgtggcg 1800
gttacctgga taccttggaa ggatccttca ccagccccaa ttacccaaag ccgcatcctg 1860
agctggctta ttgtgtgtgg cacatacaag tggagaaaga ttacaagata aaactaaact 1920
tcaaagagat tttattatgc caattcttac cggggatttt ctgcttccta cacctcaatt 1980
ttatgcagaa aacatcaaca ctacatcttt aacttgctct tctgacagga tgagagttat 2040
tataagcaaa tcctacctag aggcttttaa ctctaatggg aataacttgc aactaaaaga 2100

cccaacttgc agaccaaaat tatcaaatgt tgtggaattt tctgtccctc ttaatggatg 2160
tggtacaatc agaaaggtag aagatcagtc aattacttac accaatataa tcaccttttc 2220
tgcatcctca acttctgaag tgatcacccg tcagaaacaa ctccagatta ttgtgaagtg 2280
tgaaatggga cataattcta cagtggagat aatatacata acagaagatg atgtaataca 2340
aagtcaaaat gcactgggca aatataacac cagcatggct ctttttgaat ccaattcatt 2400
tgaaaagact atacttgaat caccatatta tgtggatttg aaccaaactc tttttgttca 2460
agttagtctg cacacctcag atccaaattt ggtggtgttt cttgatacct gtagagcctc 2520
tcccacctct gactttgcat ctccaaccta cgacctaatc aagagtggat gtagtcgaga 2580
tgaaacttgt aaggtgtatc ccttatttgg acactatggg agattccagt ttaatgcctt 2640
taaattcttg agaagtatga gctctgtgta tctgcagtgt aaagttttga tatgtgatag 2700
cagtgaccac cagtctcgct gcaatcaagg ttgtgtctcc agaagcaaac gagacatttc 2760
ttcatataaa tggaaaacag attccatcat aggacccatt cgtctgaaaa gggatcgaag 2820
tgcaagtggc aattcaggat ttcagcatga aacacatgcg gaagaaactc caaaccagcc 2880
tttcaacagt gtgcatctgt tttccttcat ggttctagct ctgaatgtgg tgactgtagc 2940
gacaatcaca gtgaggcatt ttgtaaatca acgggcagac tacaaatacc agaagctgca 3000
gaactattaa ctaacaggtc caaccctaag tgagacatgt ttctccagga tgccaaagga 3060
aatgctacct cgtggctaca catattatga ataaatgagg aagggcctga aagtgacaca 3120
caggcctgca aaaaaaaaaa aaaaaaaaaa aaa 3153

<210> 108
<211> 102
<212> PRT
<213> Homo sapiens

<400> 108
Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
50 55 60

Pro Glu Asn Lys Ala Ser Glu Leu Ser Phe Pro Met Ser Ser Leu Ile
65 70 75 80

Gln Met Glu Ala Val Lys Val Lys Thr Leu Lys Ser Leu Thr Glu Pro
85 90 95

Pro Ala Met Gly Leu Cys
100

<210> 109
<211> 1805
<212> DNA
<213> Homo sapiens

<400> 109
acgttccttc tactctggca ccactctcca ggctgccatg gggcccagca cccctctcct 60
catcttgttc cttttgtcat ggtcggggacc cctccaagga cagcagcacc accttgtgga 120
gtacatggaa cgccgactag ctgctttaga ggaacggctg gcccagtgcc aggaccagag 180
tagtcggcat gctgctgagc tgcgggactt caagaacaag atgctgccac tgctggaggt 240
ggcagagaag gagcgggagg cactcagaac tgaggccgac accatctccg ggagagtgga 300
tcgtctggag cgggaggtag actatctgga gacccagaac ccagctctgc cctgtgtaga 360
gtttgatgag aaggtgactg gaggccctgg gaccaaaggc aagggaagaa ggaatgagaa 420

gtacgatatg gtgacagact gtggctacac aatctctcaa gtgagatcaa tgaagattct 480
gaagcgattt ggtggcccag ctggtctatg gaccaaggat ccactggggc aaacagagaa 540
gatctacgtg ttagatggga cacagaatga cacagccttt gtcttcccaa ggctgcgtga 600
cttcacccttt gccatggctg cccggaaagc ttcccgagtc cgggtgccct tcccctgggt 660
aggcacaggg cagctggtat atggtggctt tctttatttt gctcggaggc ctcctggaag 720
acctggtgga ggtggtgaga tggagaacac tttgcagcta atcaaattcc acctggcaaa 780
ccgaacagtg gtggacagct cagtattccc agcagagggg ctgatccccc cctacggctt 840
gacagcagac acctacatcg acctggcagc tgatgaggaa ggtctttggg ctgtctatgc 900
cacccgggag gatgacaggc acttgtgtct ggccaagtta gatccacaga cactggacac 960
agagcagcag tgggacacac catgtcccag agagaatgct gaggctgcct ttgtcatctg 1020
tgggaccctc tatgtcgtct ataacacccg tcctgccagt cggcccgca tccagtgctc 1080
ctttgatgcc agcggcaccc tgacccctga acgggcagca ctcccttatt ttccccgcag 1140
atatggtgcc catgccagcc tccgctataa cccccgagaa cgccagctct atgcctggga 1200
tgatggctac cagattgtct ataagctgga gatgaggaag aaagaggagg aggtttgagg 1260
agctagcctt gttttttgca tctttctcac tcccatacat ttatattata tccccactaa 1320
atttcttgtt cctcattctt caaatgtggg ccagttgtgg ctcaaatcct ctatattttt 1380
agccaatggc aatcaaattc tttcagctcc tttgtttcat acggaactcc agatcctgag 1440
taatcctttt agagcccgaa gagtcaaaac cctcaatgtt ccctcctgct ctcctgcccc 1500
atgtcaacaa atttcaggct aaggatgccc cagacccagg gctctaacct tgtatgcggg 1560
caggcccagg gagcaggcag cagtgttctt cccctcagag tgacttgggg agggagaaat 1620
aggaggagac gtccagctct gtcctctctt cctcactcct cccttcagtg tcctgaggaa 1680
caggactttc tccacattgt tttgtattgc aacattttgc attaaaagga aaatccactg 1740
ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1800
aaaaa 1805

<210> 110
<211> 406
<212> PRT
<213> Homo sapiens

<400> 110
Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
1 5 10 15

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
20 25 30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
35 40 45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
50 55 60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
65 70 75 80

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
85 90 95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys
100 105 110

Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys
115 120 125

Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser
130 135 140

Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys
145 150 155 160

```
Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
                165                 170                 175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
            180                 185                 190

Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val
        195                 200                 205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg
    210                 215                 220

Pro Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
225                 230                 235                 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
                245                 250                 255

Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
            260                 265                 270

Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
        275                 280                 285

Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
    290                 295                 300

Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
305                 310                 315                 320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
                325                 330                 335

Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
            340                 345                 350

Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg
        355                 360                 365

Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
    370                 375                 380

Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg
385                 390                 395                 400

Lys Lys Glu Glu Glu Val
                405


<210> 111
<211> 2824
<212> DNA
<213> Homo sapiens

<400> 111
gtcccgcagt ggctggagcc ctgggcgctg caaagcgtgt cccgccgggt ccccgagcgt 60
cccgcgccct cgccccgcca tgctcctgct gctggggctg tgcctggggc tgtccctgtg 120
tgtggggtcg caggaagagg cgcagagctg gggccactct tcggagcagg atggactcag 180
ggtcccgagg caagtcagac tgttgcagag gctgaaaacc aaacctttga tgacagaatt 240
```

ctcagtgaag tctaccatca tttcccgtta tgccttcact acggtttcct gcagaatgct 300
gaacagagct tctgaagacc aggacattga gttccagatg cagattccag ctgcagcttt 360
catcaccaac ttcactatgc ttattggaga caaggtgtat cagggcgaaa ttacagagag 420
agaaaagaag agtggtgata gggtaaaaga gaaaaggaat aaaaccacag aagaaaatgg 480
agagaagggg actgaaatat tcagagcttc tgcagtgatt cccagcaaag acaaagccgc 540
ctttttcctg agttatgagg agcttctgca gaggcgcctg ggcaagtacg agcacagcat 600
cagcgtgcgg ccccagcagc tgtccgggag gctgagcgtg gacgtgaata tcctggagag 660
cgcgggcatc gcatccctgg aggtgctgcc gcttcacaac agcaggcaga ggggcagtgg 720
gcgcggggaa gatgattctg ggcctccccc atctactgtc attaaccaaa atgaaacatt 780
tgccaacata atttttaaac ctactgtagt acaacaagcc aggattgccc agaatggaat 840
tttgggagac tttatcatta gatatgacgt caatagagaa cagagcattg ggacatccca 900
ggttctaaat ggctattttg tgcactactt tgctcctaaa gaccttcctc ctttacccaa 960
gaatgtggta ttcgtgcttg acagcagtgc ttctatggtg ggaaccaaac tccggcagac 1020
caaggatgcc ctcttcacaa ttctccatga cctccgaccc caggaccgtt tcagtatcat 1080
tggatttccc aaccggatca aagtatggaa ggaccacttg atatcagtca ctccagacag 1140
catcagggat gggaaagtgt acattcacca tatgtcaccc actggaggta aagatgacac 1200
cttcttttca cattggcttg gctttgaaat aatgtttctt ttttttgttt ttttttttg 1260
tttttttgcc aagagataag gatttgaaag ctggggttga tggcaggaaa ggagactgca 1320
ggcgagagct ttctcagcag cttaggttgc tcggaatacc aaatccgtac tctccttttc 1380
cagtctacaa gtgaagctgg tgaagttctg gggaaaaata acctgatagg tgtttggagg 1440
cttgcctggt tcatctcatg gatcctgtta gaaaaagtct tgctgataca aaaacaatac 1500
tgtttttgta aatggttttg gggtggagaa ttacagccac gtggaccagc cagtgtttcg 1560
tgcgcacctt gggcaggggc aggtggaacg ctttgcaaaa caaggagccc tcttggtaga 1620
gctgcagcag agtgaaacag gtatcctggt ggcccgggag ggttgcggag gtaaaatgtg 1680
atggggagga tgtgggctct cagccactgc acgcttgtct tgggtgttgc ccaggtaagg 1740
gtgcagaatg ttaagagagg agagaaaaga tcataaaaat tctgagaaga gtggagaatc 1800
agagcagtgt gttaccagct gtcctagatg ttaagttctc ccaactcagg acctgcgcct 1860
tactcttgcc attccctgta tcaacagtag agtggacaca gaagaggtgc tcagtattgg 1920
agcatttagc agaacttgac ctactccctc ccccttcctt tcaggctctg tacagagaca 1980
ccacctcctg gttaattcca cttcagttat ctggaaacat acaaaacact ctgttcagtc 2040
ttctcccatc tgggattttc catctttctt atattcatgg tttcccagtc caagacaaag 2100
ccctcatttc ccaaatgaac ttaatgtgga acttgatctt gctgggccct ggtactttcc 2160
atttacactg ggatttccta ctagcctccc aaacagtata atctaggaac tgttttggtg 2220
tttgatggga gaaatagaag attagattta atatgatagt gatgctctac ggcaggaagt 2280
ccacaacacc ataaaattct tgaaggaaca gatttctctt catgtttaca tagctcctac 2340
ctccatgcac agttcctaac acagaggaca tgctcaatgg atatttgtag attggattta 2400
ttttaatggc cctgcttact agcagaatga tgtgtgtgtg ctggtggagt gggggccatg 2460
gagtaataaa cagctttaga aaatggctgg gccgggtgtg gtggctcaca cttgtaatcc 2520
cagcactttg ggaggccgag gcaggtggat cacctgaggt caggagttca agaccagcct 2580
ggccaacatg gcgaaacccc atctctacta aaaatacaaa aagttagccg ggtgtggtgg 2640
cgggtgcctg taatcccagc tacttgggag gctgaggcag gagaattgct tgaacctggg 2700
aggcagaggt tgcagtgagc caagatcatg ccagtgcact ccagcctggg tgacagcgag 2760
actctgtctc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aaaa 2824

<210> 112
<211> 399
<212> PRT
<213> Homo sapiens

<400> 112
Met Leu Leu Leu Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val Gly
1 5 10 15

Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln Asp Gly
20 25 30

Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu Lys Thr Lys
35 40 45

Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile Ile Ser Arg Tyr
50 55 60

Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn Arg Ala Ser Glu Asp
65 70 75 80

Gln Asp Ile Glu Phe Gln Met Gln Ile Pro Ala Ala Ala Phe Ile Thr
85 90 95

Asn Phe Thr Met Leu Ile Gly Asp Lys Val Tyr Gln Gly Glu Ile Thr
100 105 110

Glu Arg Glu Lys Lys Ser Gly Asp Arg Val Lys Glu Lys Arg Asn Lys
115 120 125

Thr Thr Glu Glu Asn Gly Glu Lys Gly Thr Glu Ile Phe Arg Ala Ser
130 135 140

Ala Val Ile Pro Ser Lys Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu
145 150 155 160

Glu Leu Leu Gln Arg Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val
165 170 175

Arg Pro Gln Gln Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu
180 185 190

Glu Ser Ala Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser
195 200 205

Arg Gln Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro
210 215 220

Ser Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys
225 230 235 240

Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu Gly
245 250 255

Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile Gly Asp
260 265 270

Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala Pro Lys Asp
275 280 285

Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu Asp Ser Ser Ala
290 295 300

Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys Asp Ala Leu Phe Thr
305 310 315 320

Ile Leu His Asp Leu Arg Pro Gln Asp Arg Phe Ser Ile Ile Gly Phe
325 330 335

Ser Asn Arg Ile Lys Val Trp Lys Asp His Leu Ile Ser Val Thr Pro
340 345 350

Asp Ser Ile Arg Asp Gly Lys Val Tyr Ile His His Met Ser Pro Thr
355 360 365

Gly Gly Lys Asp Asp Thr Phe Phe Ser His Trp Leu Gly Phe Glu Ile
370 375 380

Met Phe Ser Phe Phe Val Phe Phe Phe Cys Phe Phe Ala Lys Arg
385 390 395

<210> 113
<211> 1711
<212> DNA
<213> Homo sapiens

<400> 113
aggaaatgtc agaggaacca gaactcagaa ctcttcctcc tggacctttc ttcccttccc 60
ttggaggtat ccctttgaat caggcctctc tcttctcatc agtctgtagc ttccccccct 120
gtataacctg ctttcctttt tacatttatt aaaagtggat tttgtaaaag catttcattg 180
acacgcgacc tatcacagac aatggaattc gtcagtggtg gtaagactga aatcctgatg 240
cttttcacac ttcttgtctc ttgctatgta tttctgcctc tagccttgcc atgttttgcc 300
tttttttttc tttttggcca attccttttt atatgtgccc acaacagagg tggggagaca 360
cggagcaccc tgggtccttc ccagcgctgc tgggcaggcc ccgtctccag gccccagctg 420
ttgaaacttt gaagggcaac aaacaaccat ccacactgcc ggaccctagg ctgttcaggg 480
aggcagctca tttccacccc ggccccagga cacccagcct gtgccccaca aggatctctc 540
taaatgggag ggattgaggc tacttttctg ccaagcccta ttaagtagta atgtggggaa 600
acccactgtg tcagtgcagg aagccctaga caaatgtttt caaataaatt tcactgccca 660
gcctgcacag atttccattt gaagtacttc ccatccaccc tgacacccaa aggggttttt 720
ttgttttgtt ttgtttttga gacagggtct tgctttgttg cccaggctgg agtgcagtga 780
cgtggtcata gctcactgca gcctcaacct cctgggctca agtgaccctc ctgcctcagc 840
ctcccaaagt tctgagatga taggcatgag ccattgtgcc tagcctattt tgattttttt 900
cttagagtca aggtcttgct ctgttgccca ggctgatctt ggacttgcga gccaccatgc 960
ctggctgggt tttttaaaaa tagaatctca ctgatagcct gcaagaaaca gatgcagtgc 1020
ctgcttccgt atcagtccaa ggagccctcg tgtttgccac ctttaccttt gaacctcccc 1080
ctgcctccct gcctgtgtcc gcttttgcag ctcaatgcag ccatgacaag gaaagaaaag 1140
acaaaggaag gccagagagc cgcgcagttc tctgcaggtg cagatgcagg cagtggaggt 1200
ggcctgagca ggcagaagga caccaagcgc cctatgttgc ttgtcattca tgacgtggtc 1260
ttggagcttc tgactagttc agactgccac gccaacccca gaaaataccc cacatgccag 1320
aaaagtgaag tcctaggtgt ttccatctat gtttcaatct gtccatctac caggcctcgc 1380
gataaaaaca aaacaaaaaa acgctgccag gttttagaag cagttctggt ctcaaaacca 1440
tcaggatcct gccaccaggg ttcttttgaa atagtaccac atgtaaaagg gaatttggct 1500
ttcacttcat ctaataactg aattgtcagg ctttgattga taattgtaga aataagtagc 1560
cttctgttgt gggaataagt tataatcagt attcatctct ttgttttttg tcactctttt 1620
ctctctaatt gtgtcatttg tactgtttga aaaatatttc ttctataaaa ttaaactaac 1680
ctgccttaaa aaaaaaaaaa aaaaaaaaaa a 1711

<210> 114
<211> 76
<212> PRT
<213> Homo sapiens

<400> 114
Met Glu Phe Val Ser Gly Gly Lys Thr Glu Ile Leu Met Leu Phe Thr
1 5 10 15

Leu Leu Val Ser Cys Tyr Val Phe Leu Pro Leu Ala Leu Pro Cys Phe
20 25 30

Ala Phe Phe Phe Leu Phe Gly Gln Phe Leu Phe Ile Cys Ala His Asn
35 40 45

Arg Gly Gly Glu Thr Arg Ser Thr Leu Gly Pro Ser Gln Arg Cys Trp
50 55 60

Ala Gly Pro Val Ser Arg Pro Gln Leu Leu Lys Leu
65 70 75

<210> 115
<211> 2116
<212> DNA
<213> Homo sapiens

<400> 115
agtgttgggg ttgcaggaga cctaaacaca gtcaccatga agctgggctg tgtcctcatg 60
gcctgggccc tctacctttc ccttggtgtg ctctgggtgg cccagatgct actggctgcc 120
agttttgaga cgctgcagtg tgagggacct gtctgcactg aggagagcag ctgccacacg 180
gaggatgact tgactgatgc aagggaagct ggcttccagg tcaaggccta cactttcagt 240
gaacccttcc acctgattgt gtcctatgac tggctgatcc tccaaggtcc agccaagcca 300
gtttttgaag ggacctgct ggttctgcgc tgccaggcct ggcaagactg gccactgact 360
caggtgacct tctaccgaga tggctcagct ctgggtcccc ccgggcctaa cagggaattc 420
tccatcaccg tggtacaaaa ggcagacagc gggcactacc actgcagtgg catcttccag 480
agccctggtc ctgggatccc agaaacagca tctgttgtgg ctatcacagt ccaagaactg 540
tttccagcgc caattctcag agctgtaccc tcagctgaac cccaagcagg aggccccatg 600
accctgagtt gtcagacaaa gttgcccctg cagaggtcag ctgcccgcct cctcttctcc 660
ttctacaagg atggaaggat agtgcaaagc agggggctct cctcagaatt ccagatcccc 720
acagcttcag aagatcactc cgggtcatac tggtgtgagg cagccactga ggacaaccaa 780
gtttggaaac agagccccca gctagagatc agagtgcagg gtgcttccag ctctgctgca 840
cctcccacat tgaatccagc tcctcagaaa tcagctgctc caggaactgc tcctgaggag 900
gcccctgggc ctctgcctcc gccgccaacc ccatcttctg aggatccagg cttttcttct 960
cctctgggga tgccagatcc tcatctgtat caccagatgg gccttcttct caaacacatg 1020
caggatgtga gagtcctcct cggtcacctg ctcatggagt tgagggaatt atctggccac 1080
cggaagcctg ggaccacaaa ggctactgct gaatagaagt aaacagttca tccatgatct 1140
cacttaacca ccccaataaa tctgattctt tattttctct tcctgtcctg cacatatgca 1200
taagtacttt tacaagttgt cccagtgttt tgttagaata atgtagttag gtgagtgtaa 1260
ataaatttat ataaagtgag aattagagtt tagctataat tgtgtattct ctcttaacac 1320
aacagaattc tgctgtctag atcaggaatt tctatctgtt atatcgacca gaatgttgtg 1380
atttaaagag aactaatgga agtggattga atacagcagt ctcaactggg ggcaatttg 1440
ccccccagag gacattgggc aatgtttgga gacattttgg tcattatact tggggggttg 1500
ggggatggtg ggatgtgtgt gctactggca tccagtaaat agaagccagg ggtgccgcta 1560
aacatcctat aatgcacagg gcagtacccc acaacgaaaa ataatctggc ccaaaatgtc 1620
agttgtactg agtttgagaa accccagcct aatgaaaccc taggtgttgg gctctggaat 1680
gggactttgt cccttctaat tattatctct ttccagcctc attcagctat tcttactgac 1740
ataccagtct ttagctggtg ctatggtctg ttctttagtt ctagtttgta tcccctcaaa 1800
agccattatg ttgaaatcct aatccccaag gtgatggcat taagaagtgg gcctttggga 1860
agtgattaga tcaggagtgc agagccctca tgattaggat tagtgccctt atttaaaaag 1920
gccccagaga gctaactcac ccttccacca tatgaggacg tggcaagaag atgacatgta 1980
tgagaaccaa aaaacagctg tcgccaaaca ccgactctgt cgttgccttg atcttgaact 2040
tccagcctcc agaactatga gaaataaaat tctgttgttt gtaagctaaa aaaaaaaaaa 2100
aaaaaaaaaa aaaaaa 2116

<210> 116
<211> 359
<212> PRT
<213> Homo sapiens

<400> 116
Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser Leu
1 5 10 15

Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe Glu Thr
20 25 30

```
Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser Cys His Thr
        35                  40                  45

Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe Gln Val Lys Ala
    50                  55                  60

Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val Ser Tyr Asp Trp Leu
65                  70                  75                  80

Ile Leu Gln Gly Pro Ala Lys Pro Val Phe Glu Gly Asp Leu Leu Val
                85                  90                  95

Leu Arg Cys Gln Ala Trp Gln Asp Trp Pro Leu Thr Gln Val Thr Phe
            100                 105                 110

Tyr Arg Asp Gly Ser Ala Leu Gly Pro Pro Gly Pro Asn Arg Glu Phe
        115                 120                 125

Ser Ile Thr Val Val Gln Lys Ala Asp Ser Gly His Tyr His Cys Ser
    130                 135                 140

Gly Ile Phe Gln Ser Pro Gly Pro Gly Ile Pro Glu Thr Ala Ser Val
145                 150                 155                 160

Val Ala Ile Thr Val Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala
                165                 170                 175

Val Pro Ser Ala Glu Pro Gln Ala Gly Gly Pro Met Thr Leu Ser Cys
            180                 185                 190

Gln Thr Lys Leu Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser
        195                 200                 205

Phe Tyr Lys Asp Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu
    210                 215                 220

Phe Gln Ile Pro Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys
225                 230                 235                 240

Glu Ala Ala Thr Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln Leu
                245                 250                 255

Glu Ile Arg Val Gln Gly Ala Ser Ser Ser Ala Ala Pro Pro Thr Leu
            260                 265                 270

Asn Pro Ala Pro Gln Lys Ser Ala Ala Pro Gly Thr Ala Pro Glu Glu
        275                 280                 285

Ala Pro Gly Pro Leu Pro Pro Pro Pro Thr Pro Ser Ser Glu Asp Pro
    290                 295                 300

Gly Phe Ser Ser Pro Leu Gly Met Pro Asp Pro His Leu Tyr His Gln
305                 310                 315                 320

Met Gly Leu Leu Leu Lys His Met Gln Asp Val Arg Val Leu Leu Gly
                325                 330                 335

His Leu Leu Met Glu Leu Arg Glu Leu Ser Gly His Arg Lys Pro Gly
            340                 345                 350
```

Thr Thr Lys Ala Thr Ala Glu
355

<210> 117
<211> 1391
<212> DNA
<213> Homo sapiens

<400> 117
atccttggaa aagaaaatgt ttatgttgca gggtattgca tggtcacgag tgagggcagg 60
cccctgggga cacatctgcc cacagctgca caggccaggg cgcaggcaca tctgttggtt 120
ctcaggcctc agataaaacc atctccgcat catatggcca gtgaccgctt tctcccttca 180
agaaaattct gtggctgtgc agtactttga agttttaatt attaacctgc tttaattaaa 240
gcagtttcct ttcttataaa gtggaatcac caaatcttat cacacagagc acagtcctgt 300
agttacccag cccgctccag cagtgcggga gattgtaagg aagcggtggc ggctggtgaa 360
gcaagtctca catgtcggcg ttcttggcca atggatacaa agataaagaa aatgttgcct 420
ttttctagga actgtcagaa atcctcatgc ctttcaagac ttctgtgaat gacttgaatt 480
ttttattccc tgcctagggt ctgtgaacga ggcctgtctc ttccctgggg tttctttcca 540
tggcctttat ttctcctctt ccagtgggag ttttgcaggc tcttctctgt ggaaacttca 600
cgagcgttgg ctgggcctcg gcttcgctgg agtgtactcc agggtgaagg cagagtggga 660
tttgagaccc aggttaggca cgacccaggc tgagaaggga cgtttccatc attcacagtg 720
ccctccccac agcactacct caccccgacc cccaccctca ctcctacccc accccgcgat 780
cgtcaggggt gccacggtgg gccggagggt gccggctctg gctgtccctg tgccggtccc 840
tcacaaacct ctcccccttt gaaactcaag cacagctgcg aggagggcag cgaggaggga 900
cccctctctc atggttgtct ctttccccg ctatgtcata ggtagtggag gaagcgaagg 960
aagtgaacgc tgaatgtgac gcatttctga agagctcagc tgtcaccggg catagcctgg 1020
aagccccaag tctgttctga ctttgcctgg ctgtctcctt gacccgcctc ctagatcatt 1080
gtccttgatg tccaggctgg gtcatttaaa atagagatgc aatcaggaag gttgggggac 1140
ttgggactgt ggctgaattg agaccttgct gatgtattca tgtcagcacc tgagtcacag 1200
cccaggtgcc cggaagcagc ctcttcgcat aggcagtgat ttgcgattac tttaaagctc 1260
accttttttc ttcccctctc tgttcgctgc tgtcagcata atgattgtgt tccttcccta 1320
tgggatccat ctgttttgta aacaataaag cgtctgaggg agtgtaaaaa aaaaaaaaaa 1380
aaaaaaaaaa a 1391

<210> 118
<211> 56
<212> PRT
<213> Homo sapiens

<400> 118
Met Val Thr Ser Glu Gly Arg Pro Leu Gly Thr His Leu Pro Thr Ala
1 5 10 15

Ala Gln Ala Arg Ala Gln Ala His Leu Leu Val Leu Arg Pro Gln Ile
20 25 30

Lys Pro Ser Pro His His Met Ala Ser Asp Arg Phe Leu Pro Ser Arg
35 40 45

Lys Phe Cys Gly Cys Ala Val Leu
50 55

<210> 119
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 119
cttccacaga acacaagcca c 21

<210> 120
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 120
acgctcaact ccacctcc 18

<210> 121
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 121
cttggaacat agcaccactc c 21

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 122
ccattccaga cttccctgtc 20

<210> 123
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 123
gatgcagggt gtctcctgg 19

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 124
ctgtggacta cggaagggtg 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> cligonucleotide

<400> 125
gaacagatgg actctccccc 20

<210> 126
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 126
tggaggcatt gctatgtgg 19

<210> 127
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 127
tcagggagaa tgagcacatc t 21

<210> 128
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 128
ccgatcaatt ttacacaaca a 21

<210> 129
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 129
ggacacaaga agaggagagc a 21

<210> 130
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 130
tcacctcaga tgagtgtggc 20

<210> 131
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 131
acagatggat gatctgtgaa c 21

<210> 132
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 132
ggagactcac tatgaatccc t 21

<210> 133
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 133
tttaaacaca ttccctgact c 21

<210> 134
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 134
ccttgcacag cacttgacat 20

<210> 135
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 135
tgggtctcag ttaccatttg g 21

<210> 136
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 136
gtgaattagt gaagagccag c 21

<210> 137
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 137
ttctctgaaa ctgagtcccc t 21

<210> 138
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 138
tgggagtcgc ttagcctatc 20

<210> 139
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 139
agtcatgaat ggcacctggt 20

<210> 140
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 140
cataaaacag ctttccccca 20

<210> 141
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 141
aggagtttcc agggcagttt 20

<210> 142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 142
ggctcagata tagttcaggc a 21

<210> 143
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 143
aggcttatac tacggcgggt 20

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 144
gggagggaga gtttgtcctc 20

<210> 145
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 145
gcctcaccct ttggttatga 20

<210> 146
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 146

aacaggcact ttgaagtcag c 21

<210> 147
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 147
tggttggaga tgaacatccc 20

<210> 148
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 148
cctgaagatc cagcatgact t 21

<210> 149
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 149
ggcaaactgt ctaaaaagtg a 21

<210> 150
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 150
atattgcaaa tgctgcacca 20

<210> 151
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 151
cagctgcctc ctttaacagc 20

<210> 152
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 152
tcatcacacc atccatcctg 20

<210> 153
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 153
ggatccctag gctctgttcc 20

<210> 154
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 154
tggaaaaccg ttatagaccc a 21

<210> 155
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 155
ggctcaggta aacaaagatt g 21

<210> 156
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 156
aagagatcaa cgtcgggatg 20

<210> 157
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 157
ggggatttca gtttcagcaa 20

<210> 158
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 158
tcattcaaca accagaacgt g 21

<210> 159
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 159
gggctatcac tgtggctatg a 21

<210> 160
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 160
tttaattgga agagtgggcg 20

<210> 161
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 161
tacctcacgc ctgtaatccc 20

<210> 162
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 162
gaggagctat ggacgtctgc 20

<210> 163
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 163
agttcattca gccttataca a 21

<210> 164
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 164
ctaggttctg aagaggggcc 20

<210> 165
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 165
ctgaggccag ttgtttccat 20

<210> 166
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 166
ggatcagcag gattacttgc a 21

<210> 167
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 167
ttcacgcatt cttcaagcag 20

<210> 168
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 168
cctgaaatct ttggccttga 20

<210> 169
<211> 113
<212> PRT
<213> Homo sapiens

<400> 169
Met Val Leu Thr Leu Trp Cys Asn Leu Cys Ser Arg Ala Ser Ser Trp
1 5 10 15

Val Arg Gln Lys His Val Ser Cys Cys Val His Asn Tyr Thr Gln Pro
20 25 30

Phe Leu Leu Ile Gln Ser Ser Phe Trp Ala Met Ser Ser Glu Thr Lys
35 40 45

Pro Lys Ala Leu Ser Lys Asp Tyr Leu Cys Ile Ser Tyr Arg Ser Pro
50 55 60

His Ser Thr Pro Thr His Arg His Ser Ser Asn Ser Ser Tyr Asp Leu
65 70 75 80

Pro Val Glu Ala Gln Ala Ser Tyr Leu Asp Ile Lys Ser Leu His Gly
85 90 95

Gln Ser Gly Leu Cys Leu Ser Arg Phe Ile Phe His Tyr His Thr Pro
100 105 110

Tyr

<210> 170
<211> 321
<212> PRT
<213> Homo sapiens

<400> 170
Met Ala Val Ser Glu Arg Arg Gly Leu Gly Arg Gly Ser Pro Ala Glu
1 5 10 15

Trp Gly Gln Arg Leu Leu Leu Val Leu Leu Leu Gly Gly Cys Ser Gly
20 25 30

Arg Ile His Arg Leu Ala Leu Thr Gly Glu Lys Arg Ala Asp Ile Gln
35 40 45

Leu Asn Ser Phe Gly Phe Tyr Thr Asn Gly Ser Leu Glu Val Glu Leu
50 55 60

Ser Val Leu Arg Leu Gly Leu Arg Glu Ala Glu Glu Lys Ser Leu Leu
65 70 75 80

Val Gly Phe Ser Leu Ser Arg Val Arg Ser Gly Arg Val Arg Ser Tyr
85 90 95

Ser Thr Arg Asp Phe Gln Asp Cys Pro Leu Gln Lys Asn Ser Ser Ser

```
            100                 105                 110

Phe Leu Val Leu Phe Leu Ile Asn Thr Lys Asp Leu Gln Val Gln Val
        115                 120                 125

Arg Lys Tyr Gly Glu Gln Lys Thr Leu Phe Ile Phe Pro Gly Leu Leu
    130                 135                 140

Pro Glu Ala Pro Ser Lys Pro Gly Leu Pro Lys Pro Gln Ala Thr Val
145                 150                 155                 160

Pro Arg Lys Val Asp Gly Gly Gly Thr Ser Ala Ala Ser Lys Pro Lys
                165                 170                 175

Ser Thr Pro Ala Val Ile Gln Gly Pro Ser Gly Lys Asp Lys Asp Leu
            180                 185                 190

Val Leu Gly Leu Ser His Leu Asn Asn Ser Tyr Asn Phe Ser Phe His
        195                 200                 205

Val Val Ile Gly Ser Gln Ala Glu Glu Gly Gln Tyr Ser Leu Asn Phe
    210                 215                 220

His Asn Cys Asn Asn Ser Val Pro Gly Lys Glu His Pro Phe Asp Ile
225                 230                 235                 240

Thr Val Met Ile Arg Glu Lys Asn Pro Asp Gly Phe Leu Ser Ala Ala
                245                 250                 255

Glu Met Pro Leu Phe Lys Leu Tyr Met Val Met Ser Ala Cys Phe Leu
            260                 265                 270

Ala Ala Gly Ser Gly Cys Thr Ser Ser Trp Trp Arg Ala Pro Pro Trp
        275                 280                 285

Pro Ser Ser Cys Ser Arg Ala Thr Ser Ser Ser Pro Gln Glu Thr Thr
    290                 295                 300

Arg Thr Cys Ser Cys Pro Arg Arg Thr Arg Arg Met Phe Arg Trp Ser
305                 310                 315                 320

Lys


<210> 171
<211> 39
<212> PRT
<213> Homo sapiens

<400> 171
Met Gln Arg Val Glu Val Phe Ser Thr Gln Glu Leu Ala Asp Val Asn
  1               5                  10                  15

Glu Val Leu Arg Met Gly Pro Ser Pro Ile Ser Val Ala Ser Thr Glu
            20                  25                  30

Phe Cys Tyr Pro Ser Phe Arg
        35
```

<210> 172
<211> 193
<212> PRT
<213> Homo sapiens

<400> 172
Gly Trp Gly His Leu Leu Phe Leu Trp Pro Val Leu Ser Phe Val Ile
1 5 10 15

Leu Pro Leu Gly Lys Glu Cys Gln Trp Thr Asp Ala Cys Leu Ser His
20 25 30

Pro Cys Ala Asn Gly Ser Thr Cys Thr Thr Val Ala Asn Gln Phe Ser
35 40 45

Cys Lys Cys Leu Thr Gly Phe Thr Gly Gln Lys Cys Glu Thr Asp Val
50 55 60

Asn Glu Cys Asp Ile Pro Gly His Cys Gln His Gly Gly Thr Cys Leu
65 70 75 80

Asn Leu Pro Gly Ser Tyr Gln Cys Gln Cys Leu Gln Gly Phe Thr Gly
85 90 95

Gln Tyr Cys Asp Ser Leu Tyr Val Pro Cys Ala Pro Ser Pro Cys Val
100 105 110

Asn Gly Gly Thr Cys Arg Gln Thr Gly Asp Phe Thr Phe Glu Cys Asn
115 120 125

Cys Leu Pro Gly Lys Glu Leu Pro Ser Val Pro Gly Leu Gly Asp Lys
130 135 140

Pro Leu Ala Gln Glu Val Val Gly Val Ala Gln Leu Phe Phe Leu Gly
145 150 155 160

Ser Ala Arg Lys Lys Gly Ser Glu Asn Phe Val Gly Gly Gly Leu Leu
165 170 175

Val Arg Glu Glu Phe Tyr Gly Pro Thr Val Val His Lys Leu Ser Arg
180 185 190

Gly

<210> 173
<211> 72
<212> PRT
<213> Homo sapiens

<400> 173
Met Pro Ala Cys Leu Ile Pro Val Gln Met Glu Val Pro Val Pro Leu
1 5 10 15

Trp Pro Thr Ser Ser Pro Ala Asn Ala Ser Gln Ala Ser Gln Gly Arg
20 25 30

Ser Val Arg Leu Met Ser Met Ser Val Thr Phe Gln Asp Leu Pro Ala

35 40 45

Trp Trp His Leu Pro Gln Pro Ala Trp Phe Leu Pro Val Pro Val Pro
50 55 60

Ser Gly Leu His Arg Pro Val Leu
65 70

<210> 174
<211> 73
<212> PRT
<213> Homo sapiens

<400> 174
Met Leu Arg Ala Gly Ala Ala Gln Thr Cys Ser Ala Gly Leu Gln Val
1 5 10 15

Leu Lys Pro Tyr Trp Gly Trp Val Gly Ser Gly Ala Ala Ala Phe Ala
20 25 30

Thr Leu Arg Ile Gly Ala Lys Ala Thr Asp Val Tyr Leu Thr Val Thr
35 40 45

Leu His Trp Val Leu Lys Glu Ile Ile Ser Arg Cys Asn Tyr Asn Tyr
50 55 60

Cys Leu Leu Arg Lys Ile Trp Glu Phe
65 70

<210> 175
<211> 78
<212> PRT
<213> Homo sapiens

<400> 175
Met Val Leu Val Ser Ser Phe Phe Val Phe Tyr Ser Val His Ser Phe
1 5 10 15

Leu Thr Ile Trp Thr Thr Val Val Ala Asn Pro Gly Gln Trp Ile Val
20 25 30

Thr Asn Ser Val Leu Val Ala Ser Cys Phe Pro Ala Arg Ser Pro Phe
35 40 45

Val Leu Ile Met Ser Asp Thr His Ile Ser Gln Phe Cys Phe Ala Cys
50 55 60

Arg Thr Arg Lys Thr Leu Phe Pro Asn Leu Val Val Met Pro
65 70 75

<210> 176
<211> 249
<212> PRT
<213> Homo sapiens

<400> 176
Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp Phe Ala

1   5   10   15

Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala Ala Gly
            20   25   30

Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala Val Pro
        35   40   45

Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His
    50   55   60

Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe
65   70   75   80

Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu
                85   90   95

Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly
            100   105   110

Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val
        115   120   125

Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe Tyr
    130   135   140

Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr Leu Val
145   150   155   160

Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro Val Leu
                165   170   175

Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro Glu Thr
            180   185   190

Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu Cys Gly
        195   200   205

Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr Val Arg
    210   215   220

Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu Glu Glu
225   230   235   240

Ala Glu Cys Val Pro Asp Asn Cys Val
                245

<210> 177
<211> 191
<212> PRT
<213> Homo sapiens

<400> 177
Met Ile Thr Val Asp Ile Ile Pro Ser Gly Trp Asn Ser Ala Asp Gly
1   5   10   15

Lys Ser Asp Lys Thr Lys Ser Ala Pro Ser Arg Asp Pro Glu Arg Leu
            20   25   30

```
Gln Lys Ile Lys Glu Ser Leu Leu Leu Glu Asp Ser Glu Glu Glu Glu
         35                  40                  45

Gly Asp Leu Cys Arg Ile Cys Gln Met Ala Ala Ala Ser Ser Ser Asn
     50                  55                  60

Leu Leu Ile Glu Pro Cys Lys Cys Thr Gly Ser Leu Gln Tyr Val His
 65                  70                  75                  80

Gln Asp Cys Met Lys Lys Trp Leu Gln Ala Lys Ile Asn Ser Gly Ser
                 85                  90                  95

Ser Leu Glu Ala Val Thr Thr Cys Glu Leu Cys Lys Glu Lys Leu Glu
            100                 105                 110

Leu Asn Leu Glu Asp Phe Asp Ile His Glu Leu His Arg Ala His Ala
        115                 120                 125

Asn Glu Gln Ala Glu Tyr Glu Phe Ile Ser Ser Gly Leu Tyr Leu Val
    130                 135                 140

Val Leu Leu His Leu Cys Glu Gln Ser Phe Ser Asp Met Met Gly Asn
145                 150                 155                 160

Thr Asn Glu Pro Ser Thr Arg Val Arg Leu Gln Arg Met Ile Pro Lys
                165                 170                 175

Lys Thr Glu Thr Ile Thr Gly His Leu Ile Leu Pro Asn Phe Ile
            180                 185                 190


<210> 178
<211> 80
<212> PRT
<213> Homo sapiens

<400> 178
Met Phe Leu Ala Cys Leu Cys Leu Glu Asn Trp Ser Ser Gln Ala Pro
  1               5                  10                  15

Leu Ala Ala Thr Ser Pro Cys Trp Ala Ser Glu Thr Ser Leu Cys Leu
             20                  25                  30

Val Ser Tyr Tyr Ala Leu Ser Phe Ala Met Thr Thr Thr Lys Ser Lys
         35                  40                  45

Pro Val Gly Thr Pro Val Gly Pro Leu Asp Leu Pro Thr Ser Pro Gly
     50                  55                  60

Ala Cys Arg Arg Ser Pro Thr Phe Thr Ala Pro Ser Ser Asp Thr Leu
 65                  70                  75                  80


<210> 179
<211> 62
<212> PRT
<213> Homo sapiens

<400> 179
Met Pro Gly Phe Ala Gly Phe Ile Cys Leu Ile Leu Phe Cys Val Phe
```

1 5 10 15

Ser Trp Leu Phe Gly Ser Phe Pro Gly Thr Leu Asp Gly Ser Ile Pro
20 25 30

Arg His Leu Val Ile Lys Gln Leu Ser Pro Thr Pro Tyr His Gly Lys
35 40 45

Arg Gly Arg Asn Ile Ala Pro Ser Leu Ile Thr Tyr His Leu
50 55 60

<210> 180
<211> 61
<212> PRT
<213> Homo sapiens

<400> 180
Met Leu Gly Ser Leu Gly Asp Ala Arg Phe Cys Gly Phe Tyr Leu Phe
1 5 10 15

Asn Phe Ile Leu Cys Phe Leu Leu Ala Leu Trp Val Phe Pro Gly Tyr
20 25 30

Thr Arg Trp Leu His Pro Lys Ala Ser Cys His Lys Thr Ala Phe Pro
35 40 45

His Pro Ile Ser Trp Glu Lys Gly Glu Lys Tyr Ser Pro
50 55 60

<210> 181
<211> 60
<212> PRT
<213> Homo sapiens

<400> 181
Met Met Ile Ser Leu His Thr Val Gln Ser His Asn Leu Lys Ile Lys
1 5 10 15

Leu Ser Trp Leu Cys Phe Leu Cys Ser Cys Gln Asn Ile Gly Thr Ile
20 25 30

Gly Arg Ser Lys Thr Phe Ile Leu Leu Leu Gln Val Tyr Leu Gly Thr
35 40 45

Phe Thr Cys Val Phe Lys Gly Ile Ser Phe Gln Gln
50 55 60

<210> 182
<211> 227
<212> PRT
<213> Homo sapiens

<400> 182
Met Met Gly Ser Glu Ala Ala Gly Arg Gly Ser Gln Glu Leu Leu Val
1 5 10 15

Val Gln Pro Val Leu Pro Ser Glu Ala Leu Leu Phe Pro Gly Leu Pro

```
            20                  25                  30

Ala Gly Phe Ser Arg Arg Leu Ser Ser Asn Ala Gly Pro Arg Leu Leu
        35                  40                  45

Ala Trp Val Leu Ala Cys Pro Leu Arg Pro Leu Ala Ala Cys Leu Leu
    50                  55                  60

Ser Leu Val Ala Leu Pro Gly Cys Trp Ala Ala Leu Ser Gly Arg Leu
65                  70                  75                  80

Leu Pro Val Cys Phe Pro Trp Trp Leu Cys Leu Gly Ala Gly Pro Ala
                85                  90                  95

Phe Ser Gly Cys Leu Leu Pro Val Tyr Cys His Leu Gln Arg Gly Ser
            100                 105                 110

Leu Leu Arg Pro Thr Leu Leu His Leu Ala Pro Pro Trp Leu Leu Ala
        115                 120                 125

Trp Pro Asn Leu Ala Phe Cys Ala Met Leu Glu Leu Glu Leu Leu Leu
    130                 135                 140

Phe Phe Arg Gly Gly Asn Arg Val Glu Ser Gly Lys Gly Leu Ala Pro
145                 150                 155                 160

Lys Cys Cys Cys Cys Gly Phe Phe Ala Phe Ser Lys Asp Ala Leu Pro
                165                 170                 175

Gly Pro Lys Leu Gln Thr Ala Val Leu Ser Lys Gln Val Arg Ser Leu
            180                 185                 190

Gly Phe Gly Ala His Leu Leu Ser Gly Ser Ile Ser Ile Leu Leu Leu
        195                 200                 205

Ala Thr Ser Gly Gln Arg Pro Pro Gln Pro His Ile Ala Arg Cys Trp
    210                 215                 220

Gln Lys Gly
225


<210> 183
<211> 97
<212> PRT
<213> Homo sapiens

<400> 183
Met Leu Ser Cys Thr Leu Gly Leu Thr Val Cys Pro Leu Ser Pro Ala
  1               5                  10                  15

Pro Ser Val Thr Leu Ala Val Ala Leu Asn Gly Gln Leu Arg Arg Pro
            20                  25                  30

Leu Cys Cys Ser Ser Ala Phe Pro Glu Val Gly Glu Pro Ala Trp Pro
        35                  40                  45

Arg Pro Leu Ser Ser Asp Gln Ala Leu Ser Pro Arg Ser Tyr Gly Arg
    50                  55                  60
```

Pro Gly Ser Gly Val Gly Thr His Gly Pro Gly Trp Gly Gly Ala Gln
65 70 75 80

Ser Asp Val Asn Phe Phe Pro Cys Val Asp Met Tyr Ser Gln Arg Val
85 90 95

Val

<210> 184
<211> 68
<212> PRT
<213> Homo sapiens

<400> 184
Met Cys Phe Leu Leu Phe Gly Ser Leu Cys Ile Tyr Tyr Phe Ser Leu
1 5 10 15

Phe Leu Val Phe Phe Phe Ser Cys Phe Cys Phe Val Trp Cys Phe Val
20 25 30

Pro Val Phe Ile Val Ser Gly Ile Ser Leu Pro Leu Trp Ile Pro His
35 40 45

Gly Leu Asp Arg Asp Gly Pro Val Met Pro Ser Ser Phe Leu Leu Leu
50 55 60

Leu Leu Leu Trp
65

<210> 185
<211> 142
<212> PRT
<213> Homo sapiens

<400> 185
Met Phe Ser Cys Asn Glu Asn Ser Ile Phe Phe Arg Ile Gly Phe Val
1 5 10 15

Phe Ile Leu Leu Ser Phe Ile Ser Ser Cys Gln Thr Leu Asn Gly Tyr
20 25 30

Val Cys Ile Leu Ile Thr Leu Phe Ser Leu Leu Trp Lys Arg Arg Thr
35 40 45

Arg Glu Gln Met Leu Leu Arg Ala Gly Val Ser Glu Lys Asn Leu Ser
50 55 60

Met Leu Phe Asn Val Phe Leu Pro Leu Pro His Ser Val Cys Val Thr
65 70 75 80

Phe Tyr Asn Ile Lys Lys Tyr Tyr Asn Ile Ser Arg Ile Trp Asn Cys
85 90 95

His His Asp Glu Trp Pro Phe Gln Cys Ile Val Thr Glu Ile Pro Glu
100 105 110

Asp Ser Pro Gly Leu Gln Phe His Trp Phe Leu Leu Gln Phe Leu Val

115 120 125

Ala Val Ile Val Ala Val Ser Ser Leu Lys Asp Leu Leu Trp
130 135 140

<210> 186
<211> 111
<212> PRT
<213> Homo sapiens

<400> 186
Met Ser Cys Pro Leu Pro Leu Leu Ile Ser Ala Ile Ala Ala Val Gly
1 5 10 15

Ser Ser Met Gln Thr His Ala Arg Ala Ser Phe Ala Ala Gly Pro Ser
20 25 30

Gln Glu Asp Phe Ser Ala His Leu Ala Gln Asp Gln His Ser Pro Glu
35 40 45

Val Gln Gly His Tyr His Ala Arg Gly Asn Pro Pro Ala Val Gly Asp
50 55 60

Thr Ser Leu Trp Met Lys Val Pro Thr Ser His His Ser Asp Glu Lys
65 70 75 80

His Gln Glu Ala Ser Cys Thr Phe Leu Lys Arg Pro Gln Gln Asp Gln
85 90 95

Ser Pro Ile Ala His Ser Ser His Leu Asn Asn Ala Pro Phe Tyr
100 105 110

<210> 187
<211> 72
<212> PRT
<213> Homo sapiens

<400> 187
Met Phe Gly Met Pro His Thr Met Ser Cys Pro Leu Pro Leu Leu Ile
1 5 10 15

Ser Ala Ile Ala Ala Val Gly Ser Ser Met Gln Thr His Ala Arg Ala
20 25 30

Ser Phe Ala Ala Gly Pro Ser Gln Lys Thr Ser Gln Pro Ile Trp Ser
35 40 45

Arg Ile Phe Leu Pro Leu Lys Val Thr Ala Pro Lys Ser Cys Pro Met
50 55 60

Phe Tyr Phe Gln Glu Phe Pro Asn
65 70

<210> 188
<211> 109
<212> PRT
<213> Homo sapiens

<400> 188
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
50 55 60

Tyr Leu Glu Thr Gly Met Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Arg Pro
85 90 95

Gln Gln Arg Arg Gln Arg Pro Pro Arg Cys Gly Arg Pro
100 105

<210> 189
<211> 76
<212> PRT
<213> Homo sapiens

<400> 189
Met Trp Pro Ala Leu His Leu Leu His His Trp Ala Val Trp Gly Cys
1 5 10 15

Arg Leu His His His His Asp Pro Pro Pro Gly Leu Cys His Pro Ser
20 25 30

Phe Leu Pro Ser Leu Trp Pro His Cys His Cys Gly Gly Arg Ala Gly
35 40 45

Gly Gly Cys Gly Leu Cys Cys Pro Pro Ala Gln Ser Leu Arg Ala Gly
50 55 60

Pro Ser Lys Ala Thr Gly Lys Glu Gly Cys Ala Cys
65 70 75

<210> 190
<211> 168
<212> PRT
<213> Homo sapiens

<400> 190
Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys Gly
1 5 10 15

Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu Val
20 25 30

Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile Leu
35 40 45

Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg Leu
50 55 60

Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Glu Trp Leu
65 70 75 80

Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser Val Thr Thr Gln Ala
85 90 95

Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala Met Leu Gln Ala Cys
100 105 110

Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys Gln Phe Val Glu Gln
115 120 125

His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg Gly Trp Asp Ala His
130 135 140

Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr Met Ser Ser Pro Leu
145 150 155 160

Gln Cys Ile His Ser Pro Asp Leu
165

<210> 191
<211> 272
<212> PRT
<213> Homo sapiens

<400> 191
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Leu Ser Glu Gln Gln Phe
85 90 95

Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg
100 105 110

Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln
115 120 125

Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu
130 135 140

Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met

145 150 155 160

Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met Asp Asp
165 170 175

Ser Ala Gly Pro Arg Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu
180 185 190

Cys Met Ser Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile
195 200 205

Pro Gln Ala Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu
210 215 220

Lys Cys Lys Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu
225 230 235 240

Val Pro Arg Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val
245 250 255

Cys Gly Thr Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu
260 265 270

<210> 192
<211> 60
<212> PRT
<213> Homo sapiens

<400> 192
Met Pro Pro Ser Ala Phe Leu Phe Phe Phe Trp Arg Gln Ser Leu Ala
1 5 10 15

Leu Leu Pro Arg Leu Glu Cys Ser Ser Thr Ile Ser Ala Leu Thr Ala
20 25 30

Thr Ser Val Ser Trp Val Gln Ala Ile Leu Leu Pro Gln Pro Pro Lys
35 40 45

Tyr Leu Gly Leu Gln Ala Cys Ala Thr Thr Pro Gly
50 55 60

<210> 193
<211> 357
<212> PRT
<213> Homo sapiens

<400> 193
Met Pro Ile Leu Thr Gly Asp Phe Leu Leu Pro Thr Pro Gln Phe Tyr
1 5 10 15

Ala Glu Asn Ile Asn Thr Thr Ser Leu Thr Cys Ser Ser Asp Arg Met
20 25 30

Arg Val Ile Ile Ser Lys Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly
35 40 45

Asn Asn Leu Gln Leu Lys Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn
50 55 60

```
Val Val Glu Phe Ser Val Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys
65                  70                  75                  80

Val Glu Asp Gln Ser Ile Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala
                85                  90                  95

Ser Ser Thr Ser Glu Val Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile
            100                 105                 110

Val Lys Cys Glu Met Gly His Asn Ser Thr Val Glu Ile Ile Tyr Ile
        115                 120                 125

Thr Glu Asp Asp Val Ile Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn
    130                 135                 140

Thr Ser Met Ala Leu Phe Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu
145                 150                 155                 160

Glu Ser Pro Tyr Tyr Val Asp Leu Asn Gln Thr Leu Phe Val Gln Val
                165                 170                 175

Ser Leu His Thr Ser Asp Pro Asn Leu Val Val Phe Leu Asp Thr Cys
            180                 185                 190

Arg Ala Ser Pro Thr Ser Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile
        195                 200                 205

Lys Ser Gly Cys Ser Arg Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe
    210                 215                 220

Gly His Tyr Gly Arg Phe Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser
225                 230                 235                 240

Met Ser Ser Val Tyr Leu Gln Cys Lys Val Leu Ile Cys Asp Ser Ser
                245                 250                 255

Asp His Gln Ser Arg Cys Asn Gln Gly Cys Val Ser Arg Ser Lys Arg
            260                 265                 270

Asp Ile Ser Ser Tyr Lys Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile
        275                 280                 285

Arg Leu Lys Arg Asp Arg Ser Ala Ser Gly Asn Ser Gly Phe Gln His
    290                 295                 300

Glu Thr His Ala Glu Glu Thr Pro Asn Gln Pro Phe Asn Ser Val His
305                 310                 315                 320

Leu Phe Ser Phe Met Val Leu Ala Leu Asn Val Val Thr Val Ala Thr
                325                 330                 335

Ile Thr Val Arg His Phe Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln
            340                 345                 350

Lys Leu Gln Asn Tyr
        355
```

<210> 194

<211> 169
<212> PRT
<213> Homo sapiens

<400> 194
Met Gln Cys Leu Leu Pro Tyr Gln Ser Lys Glu Pro Ser Cys Leu Pro
1   5   10   15

Pro Leu Pro Leu Asn Leu Pro Leu Pro Pro Cys Leu Cys Pro Leu Leu
            20   25   30

Gln Leu Asn Ala Ala Met Thr Arg Lys Glu Lys Thr Lys Glu Gly Gln
        35   40   45

Arg Ala Ala Gln Phe Ser Ala Gly Ala Asp Ala Gly Ser Gly Gly Gly
    50   55   60

Leu Ser Arg Gln Lys Asp Thr Lys Arg Pro Met Leu Leu Val Ile His
65   70   75   80

Asp Val Val Leu Glu Leu Leu Thr Ser Ser Asp Cys His Ala Asn Pro
                85   90   95

Arg Lys Tyr Pro Thr Cys Gln Lys Ser Glu Val Leu Gly Val Ser Ile
            100   105   110

Tyr Val Ser Ile Cys Pro Ser Thr Arg Pro Arg Asp Lys Asn Lys Thr
        115   120   125

Lys Lys Arg Cys Gln Val Leu Glu Ala Val Leu Val Ser Lys Pro Ser
    130   135   140

Gly Ser Cys His Gln Gly Ser Phe Glu Ile Val Pro His Val Lys Gly
145   150   155   160

Asn Leu Ala Phe Thr Ser Ser Asn Asn
                165

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/07285

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :C12Q 1/68; C12N 15/00, 15/09, 15/63, 15/86
US CL :435/6, 69.1, 69.3, 320.1, 455, 471; 530/300, 350; 424/189.1
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 69.1, 69.3, 320.1, 455, 471; 530/300, 350; 424/189.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EAST, USPATFULL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X -- Y	Database EST on STN. Hudson et al. AN X11582. 'New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease' WO 98/20165 see, bases 1-67, which would hybridize to SEQ ID NO: 1.	1 -- 2-11
X -- Y	Database EST on STN. Hillier et al. AN W51776. 'The WashU-Merck EST Project' 11 October 1996. See Sequence Alignment (attached) disclosing 85% similarity to SEQ ID NO: 1, and would hybridize to SEQ ID NO: 1	1 -- 2-11
X -- Y	Database EST on STN. 'NCI-CGAP' AN AA568724. '09 September 1997. See Sequence Alignment (attached) which discloses a polynucleotide with 88% similarity to SEQ ID NO: 1 and would hybridize to SEQ ID NO: 1.	1 -- 2-11

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
27 JUNE 2000	19 JUL 2000

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	MARY K ZEMAN
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No. PCT/US00/07285

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- Y, P	Database Gen EMBL. AN AC009651. Birren et al. 'Homo sapiens chromosome 11, clone' 29 September 1999. See Sequence Alignment (attached) which discloses a polynucleotide having up to 98% identity to SEQ ID NO: 1, and could encode SEQ ID NO: 2.	1 -- 2-11

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/07285

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11, SEQ ID NO: 1 and 2

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s)1-11, drawn to polynucleotides (SEQ ID NO: 1) and encoded polypeptides (SEQ ID NO: 2), and methods of making the recombinant polypeptides.
Group II, claim(s) 12-13, drawn to polynucleotides (SEQ ID NO: 3) and encoded polypeptides (SEQ ID NO: 4).
Group III, claim(s) 14-15, drawn to polynucleotides (SEQ ID NO: 5) and encoded polypeptides (SEQ ID NO: 6).
Group IV, claim(s)16-17, drawn to polynucleotides (SEQ ID NO: 7) and encoded polypeptides (SEQ ID NO: 8).
Group V, claim(s) 18-19, drawn to polynucleotides (SEQ ID NO: 9) and encoded polypeptides (SEQ ID NO: 10).
Group VI, claim(s) 20-21, drawn to polynucleotides (SEQ ID NO: 11) and encoded polypeptides (SEQ ID NO: 12).
Group VII, claim(s)22-23, drawn to polynucleotides (SEQ ID NO: 13) and encoded polypeptides (SEQ ID NO: 14).
Group VIII, claim(s) 24-25, drawn to polynucleotides (SEQ ID NO: 15) and encoded polypeptides (SEQ ID NO: 16).
Group IX, claim(s) 26-27, drawn to polynucleotides (SEQ ID NO: 17) and encoded polypeptides (SEQ ID NO: 18).
Group X, claim(s)28-29, drawn to polynucleotides (SEQ ID NO: 19) and encoded polypeptides (SEQ ID NO: 20).
Group XI, claim(s)30-31, drawn to polynucleotides (SEQ ID NO: 21) and encoded polypeptides (SEQ ID NO: 22).
Group XII, claim(s) 32-33, drawn to polynucleotides (SEQ ID NO: 23) and encoded polypeptides (SEQ ID NO: 24).
Group XIII, claim(s) 34-35, drawn to polynucleotides (SEQ ID NO: 25) and encoded polypeptides (SEQ ID NO: 26).
Group XIV, claim(s) 36-37, drawn to polynucleotides (SEQ ID NO: 27) and encoded polypeptides (SEQ ID NO: 28).
Group XV, claim(s) 38-39, drawn to polynucleotides (SEQ ID NO: 29) and encoded polypeptides (SEQ ID NO: 30).
Group XVI, claim(s) 40-41, drawn to polynucleotides (SEQ ID NO: 31) and encoded polypeptides (SEQ ID NO: 32).
Group XVII, claim(s)42-43, drawn to polynucleotides (SEQ ID NO: 33) and encoded polypeptides (SEQ ID NO: 34).
Group XVIII, claim(s) 44-45, drawn to polynucleotides (SEQ ID NO: 35) and encoded polypeptides (SEQ ID NO: 36).
Group XIX, claim(s) 46-47, drawn to polynucleotides (SEQ ID NO: 37) and encoded polypeptides (SEQ ID NO: 38).
Group XX, claim(s) 48-49, drawn to polynucleotides (SEQ ID NO: 39) and encoded polypeptides (SEQ ID NO: 40).
Group XXI, claim(s)50-51, drawn to polynucleotides (SEQ ID NO: 41) and encoded polypeptides (SEQ ID NO: 42).
Group XXII, claim(s) 52-53, drawn to polynucleotides (SEQ ID NO: 43) and encoded polypeptides (SEQ ID NO: 44).
Group XXIII, claim(s) 54-55, drawn to polynucleotides (SEQ ID NO: 45) and encoded polypeptides (SEQ ID NO: 46).
Group XXIV, claim(s)56-57, drawn to polynucleotides (SEQ ID NO: 47) and encoded polypeptides (SEQ ID NO: 48).
Group XXV, claim(s) 58-59, drawn to polynucleotides (SEQ ID NO: 49) and encoded polypeptides (SEQ ID NO: 50).
Group XXVI, claim(s) 60-61, drawn to polynucleotides (SEQ ID NO: 51) and encoded polypeptides (SEQ ID NO: 52).
Group XXVII, claim(s)62-63, drawn to polynucleotides (SEQ ID NO: 53) and encoded polypeptides (SEQ ID NO: 54).
Group XXVIII, claim(s) 64-65, drawn to polynucleotides (SEQ ID NO: 55) and encoded polypeptides (SEQ ID NO: 56).
Group XXIX, claim(s) 66-67, drawn to polynucleotides (SEQ ID NO: 57) and encoded polypeptides (SEQ ID NO: 58).
Group XXX, claim(s)68-69, drawn to polynucleotides (SEQ ID NO: 59) and encoded polypeptides (SEQ ID NO: 60).
Group XXXI, claim(s)70-71, drawn to polynucleotides (SEQ ID NO: 61) and encoded polypeptides (SEQ ID NO: 62).
Group XXXII, claim(s) 72-73, drawn to polynucleotides (SEQ ID NO: 63) and encoded polypeptides (SEQ ID NO: 64).
Group XXXIII, claim(s) 74-75, drawn to polynucleotides (SEQ ID NO: 5) and encoded polypeptides (SEQ ID NO: 66).
Group XXXIV, claim(s) 76-77, drawn to polynucleotides (SEQ ID NO: 67) and encoded polypeptides (SEQ ID NO: 68).
Group XXXV, claim(s) 78-79, drawn to polynucleotides (SEQ ID NO: 69) and encoded polypeptides (SEQ ID NO: 70).
Group XXXVI, claim(s) 80-81, drawn to polynucleotides (SEQ ID NO: 71) and encoded polypeptides (SEQ ID NO: 72).
Group XXXVII, claim(s)82-83, drawn to polynucleotides (SEQ ID NO: 73) and encoded polypeptides (SEQ ID NO: 74).
Group XXXVIII, claim(s) 84-85, drawn to polynucleotides (SEQ ID NO: 75) and encoded polypeptides (SEQ ID NO: 76).
Group XXXIX, claim(s) 86-87, drawn to polynucleotides (SEQ ID NO: 77) and encoded polypeptides (SEQ ID NO: 78).
Group XXXX, claim(s) 88-89, drawn to polynucleotides (SEQ ID NO: 79) and encoded polypeptides (SEQ ID NO: 80).
Group XXXXI, claim(s)90-91, drawn to polynucleotides (SEQ ID NO: 81) and encoded polypeptides (SEQ ID NO: 82).
Group XXXXII, claim(s) 92-93, drawn to polynucleotides (SEQ ID NO: 83) and encoded polypeptides (SEQ ID NO: 84).
Group XXXXIII, claim(s) 94-95, drawn to polynucleotides (SEQ ID NO: 85) and encoded polypeptides (SEQ ID NO:

86).
Group XXXXIV, claim(s)96-97, drawn to polynucleotides (SEQ ID NO: 87) and encoded polypeptides (SEQ ID NO: 88).
Group XXXXV, claim(s) 98-99, drawn to polynucleotides (SEQ ID NO: 89) and encoded polypeptides (SEQ ID NO: 90).
Group XXXXVI, claim(s) 100-101, drawn to polynucleotides (SEQ ID NO: 91) and encoded polypeptides (SEQ ID NO: 92).
Group XXXXVII, claim(s) 102-103, drawn to polynucleotides (SEQ ID NO: 93) and encoded polypeptides (SEQ ID NO: 94).
Group XXXXVIII, claim(s) 104-105, drawn to polynucleotides (SEQ ID NO: 95) and encoded polypeptides (SEQ ID NO: 96).
Group XXXXIX, claim(s) 106-107, drawn to polynucleotides (SEQ ID NO: 97) and encoded polypeptides (SEQ ID NO: 98).
Group L, claim(s) 108-109, drawn to polynucleotides (SEQ ID NO: 99) and encoded polypeptides (SEQ ID NO: 100).
Group LI, claim(s)101-111, drawn to polynucleotides (SEQ ID NO: 101) and encoded polypeptides (SEQ ID NO: 102).
Group LII, claim(s) 112-113, drawn to polynucleotides (SEQ ID NO: 103) and encoded polypeptides (SEQ ID NO: 104).
Group LIII, claim(s) 114-115, drawn to polynucleotides (SEQ ID NO: 105) and encoded polypeptides (SEQ ID NO: 106).
Group LIV, claim(s)116-117, drawn to polynucleotides (SEQ ID NO: 107) and encoded polypeptides (SEQ ID NO: 108).
Group LV, claim(s) 118-119, drawn to polynucleotides (SEQ ID NO: 109) and encoded polypeptides (SEQ ID NO: 110).
Group LVI, claim(s) 120-121, drawn to polynucleotides (SEQ ID NO: 111) and encoded polypeptides (SEQ ID NO: 112).
Group LVII, claim(s)122-123, drawn to polynucleotides (SEQ ID NO: 113) and encoded polypeptides (SEQ ID NO: 114).
Group LVIII, claim(s) 124-125, drawn to polynucleotides (SEQ ID NO: 115) and encoded polypeptides (SEQ ID NO: 116).
Group LIX, claim(s) 126-127, drawn to polynucleotides (SEQ ID NO: 117) and encoded polypeptides (SEQ ID NO: 118).

The inventions listed as Groups ONE (I) to FIFTY NINE (LIX) do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each polynucleotide and corresponding polypeptide do not share any sequence homology, similar structure or other feature which could be considered a special technical feature. Each polynucleotide sequence and corresponding polypeptide sequence is a separate and distinct invention, having no obvious shared features, and thus, lack unity under PCT Rule 13.2.